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Sequence Listing

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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

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 caataccac agtggcctct tccccacct gggcgtattc acgctgggag 1400
 ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450
 gggaagcagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500
 tgtcagaacg cacctgctgc ggcactccga gccagtaag ctcacctttg 1550
 tgggggagct tgcccacggc cgcttcagtg ccaagatgga ccacctggtg 1600
 tgcttctctg cagggacgct ggctctgggc gtctaccacg gcctgccgcg 1650
 cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700
 accggcagat ggagacgggg ctgagtcccg agatcgtgca cttcaacctt 1750
 tacccccagc cgggccgtcg ggacgtggag gtcaagccag cagacaggca 1800
 caacctgctg cggccagaga ccgtggagag cctgtttctac ctgtaccgag 1850
 tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900
 ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950
 tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000
 tcttggggga gacgtcaag tatctgttct tgctcttctc cgatgacca 2050
 aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccaccctct 2100

gcctatctgg acccctgcct aggggtggatg gctgctgggtg tggggacttc 2150
 ggggtgggcag aggcaccttg ctgggtctgt ggcattttcc aagggccccac 2200
 gtagcaccgg caaccgcaa gtggcccagg ctctgaactg gctctgggct 2250
 cctcctcgtc tctgctttaa tcaggacacc gtgaggacaa gtgaggccgt 2300
 cagtcttgggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350
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 gtctctgtgg gccgaccaga ggggggcttc gaggtgggtcc ctggtactgg 2450
 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctcgtgaagc 2500
 ctcagatgtc cccaatccaa gggctctggag gggctgccgt gactccagag 2550
 gcctgaggct ccagggctgg ctctgggtgt tacaagctgg actcagggat 2600
 cctcctggcc gccccgcagg gggcttggag ggctggacgg caagtccgtc 2650
 tagctcacgg gccctccag tggaatgggt cttttcgggtg gagataaaag 2700
 ttgatttgct ctaaccgcaa 2720

<210> 12
 <211> 699
 <212> PRT
 <213> Homo sapiens

<220>
 <221> TRANSMEM
 <222> 21-40 and 84-105
 <223> Transmembrane Domain (type II)

<400> 12
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser
 1 5 10 15
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
 20 25 30
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys
 110 115 120
 Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val
 125 130 135
 Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro
 140 145 150
 Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro
 155 160 165
 Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly
 170 175 180
 Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro
 185 190 195
 Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly
 200 205 210
 Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg
 215 220 225
 Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln
 230 235 240
 Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp
 245 250 255
 Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly
 260 265 270
 His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe
 275 280 285
 Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile
 290 295 300
 Leu Gly Leu Arg Lys Glu Phe Glu Glu Ala Arg Lys Trp Val Ser
 305 310 315
 Lys Lys Leu His Phe Glu Lys Asp Val Asp Val Asn Leu Phe Glu
 320 325 330
 Ser Thr Ile Arg Ile Leu Gly Gly Leu Leu Ser Ala Tyr His Leu
 335 340 345
 Ser Gly Asp Ser Leu Phe Leu Arg Lys Ala Glu Asp Phe Gly Asn
 350 355 360
 Arg Leu Met Pro Ala Phe Arg Thr Pro Ser Lys Ile Pro Tyr Ser
 365 370 375
 Asp Val Asn Ile Gly Thr Gly Val Ala His Pro Pro Arg Trp Thr
 380 385 390
 Ser Asp Ser Thr Val Ala Glu Val Thr Ser Ile Gln Leu Glu Phe

395 400 405
 Arg Glu Leu Ser Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala
 410 415 420
 Val Glu Lys Val Thr Gln His Ile His Gly Leu Ser Gly Lys Lys
 425 430 435
 Asp Gly Leu Val Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe
 440 445 450
 Thr His Leu Gly Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr
 455 460 465
 Tyr Glu Tyr Leu Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu
 470 475 480
 Thr Gln Leu Leu Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg
 485 490 495
 Thr His Leu Leu Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val
 500 505 510
 Gly Glu Leu Ala His Gly Arg Phe Ser Ala Lys Met Asp His Leu
 515 520 525
 Val Cys Phe Leu Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly
 530 535 540
 Leu Pro Ala Ser His Met Glu Leu Ala Gln Glu Leu Met Glu Thr
 545 550 555
 Cys Tyr Gln Met Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu
 560 565 570
 Ile Val His Phe Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val
 575 580 585
 Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr
 590 595 600
 Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys
 605 610 615
 Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe
 620 625 630
 Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln
 635 640 645
 Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe
 650 655 660
 Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp
 665 670 675
 Pro Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala
 680 685 690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

B1
<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgcgt aggcccgga ggccgggccg gccgggctgc gagcgctgc 50
cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaagcg 100
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150
ccctcggaag tgttcgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300
 cccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350
 cccaccgect ggcagtgtg gtgcccttcc gcgaacgctt cgaggagctc 400
 ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450
 gcaccacatc tacgtgtcga accaggtgga ccacttcagg ttcaaccggg 500
 cagcgctcat caacgtgggc ttcttgaga gcagcaacag cacggactac 550
 attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600
 tggctttcct gaggtgggc ccttcacgt ggctccccg gagctccacc 650
 ctctctacca ctacaagacc tatgtcggcg gcatcctgct gctctccaag 700
 cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750
 ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
 ttttcgccc ctcggaatc acaactgggt acaagacatt tcgccacctg 850
 catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900
 acaggagcag ttcaagtgga acaggaggagg aggcctgaac actgtgaagt 950
 accatgtggc ttcccgcaact gccctgtctg tgggcggggc cccctgcact 1000
 gtctcaaca tcatgttga ctgtgacaag accgccacac cctggtgcac 1050
 attcagctga gctggatgga cagtgaggaa gcctgtacct acaggccata 1100
 ttgctcaggc tcaggacaag gcctcaggtc gtgggcccag ctctgacagg 1150
 atgtggagtg gccaggacca agacagcaag ctacgcaatt gcagccacc 1200
 ggccgccaag gcaggcttgg gctgggccag gacacgtggg gtgcctggga 1250
 cgctgcttgc catgcacagt gatcagagag aggtgggggt gtgtcctgtc 1300
 cgggaccccc cctgccttcc tgctcaccct actctgacct ccttcacgtg 1350
 cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400
 cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggc 1450
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens
 <220>

<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

 <220>
 <221> misc_feature
 <222> 19-25, 65-71, 247-253, 285-291, 303-310
 <223> N-myristoylation site.

 <220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

B1

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1 5 10 15

 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
 20 25 30

 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45

 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
 50 55 60

 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
 65 70 75

 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
 80 85 90

 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
 95 100 105

 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
 110 115 120

 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
 125 130 135

 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

140 145 150
 Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp
 155 160 165
 Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala
 170 175 180
 Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His
 185 190 195
 Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His
 200 205 210
 Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly
 215 220 225
 Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
 230 235 240
 Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe
 245 250 255
 Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg
 260 265 270
 Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly
 275 280 285
 Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu
 290 295 300
 Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp
 305 310 315
 Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser
 320 325

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
 gcgaacgctt cgaggagtcc tgg 23

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcggcc 200
tgccatgacc tgcagccaag cccagccccg tggggaaggg gagaaagtgg 250
gggatggcta agaaagctgg gagatagggg acagaagagg gtagtgggtg 300
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450
taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15
Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30
Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45
Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

gggacccatg cggccgtgac ccccggtctc ctagaggccc agcgcagccg 50
cagcggacaa aggagcatgt ccgcgcgggg gaaggcccg cctccggccg 100
ccataaggct ccggtcgccg ctggggccgc gccgcgctcc tgcccgcccg 150
ggctccgggg cggcccgcta ggccagtgcg ccgcgcgctc cccgcagggc 200
cccgggccgc agcatggagc cacccgagc ccggcggggc cgcgcgcagc 250
cgccgctgtt gctgcgcgc tcgctgttag cgctgctgc gctgctggga 300
ggcggcgggc gcggcggcgc cgcggcgctg cccgcgggt gcaagcacga 350
tgggcggccc cgaggggctg gcagggcggc gggcgccgc gagggcaagg 400
tggtgtgcag cagcctggaa ctgcgcagc tcctgcccgc agatactctg 450
cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500
gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600
tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650
agacatattt cgaggactca ccaatctggt tcggctaaac ctttcgggga 700
atattgtttt ttcatatct caaggaactt ttgattatct tgcgtcatta 750
cggctcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800
gtggatgcat cgctgggtaa aggagaagaa catcacgcta cgggatacca 850

ggtgtgttta tcctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900
 caggagctgt tgacatgcga ccctccgctt gaattgccgt ctttctacat 950
 gactccatct catcgccaag ttgtgtttga aggagacagc cttcctttcc 1000
 agtgcacggc ttcataatatt gatcaggaca tgcaagtgtt gtggtatcag 1050
 gatgggagaa tagttgaaac cgatgaatcg caaggtattt ttgttgaaaa 1100
 gaacatgatt cacaactgct ccttgattgc aagtgcccta accatttcta 1150
 atattcaggc tggatctact ggaaattggg gctgtcatgt ccagaccaa 1200
 cgtgggaata atacaggagc tgtggatatt gtggtattag agagtctctg 1250
 acagtactgt cctccagaga ggggtgtaaa caacaagggt gacttcagat 1300
 ggcccagAAC attggcaggc attactgcat atctgcagtg tacgcggaac 1350
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 ttggcgcaga tgtgatagag gtggcttttg ggcagatgat gattattctc 1450
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 atgcccctca atcttaccaa tgccgtggca acagctcgac agttactggc 1550
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 aaagagctag gtgacgtgat ggttgacatt gcaagtaaca tcatgttggc 1700
 tgatgaacgt gtcctgtggc tggcgcagag ggaagctaaa gcctgcagta 1750
 ggattgtgca gtgtcttcag cgcattgcta cctaccggct agccggtgga 1800
 gctcacgttt attcaacata ttcaccaat attgctctgg aagcttatgt 1850
 catcaagtct actggcttca cggggatgac ctgtaccgtg ttccagaaag 1900
 tggcagcctc tgatcgtaca ggactttcgg attatgggag gcgggatcca 1950
 gagggaaacc tggataagca gctgagcttt aagtgcaatg tttcaaatac 2000
 attttcgagt ctggcactaa aggtatgtta cattctgcaa tcatttaaga 2050
 ctatttacag ttaaattaga atgctccaaa tgttctgctt cgcaaaataa 2100
 ccttattaaa agattttttt ttgcaggaag ataggtatta ttgcttttgc 2150
 tactgtttta aagaaaacta accaggaaga actgcattac gactttcaag 2200
 ggccctaggc atttttgcct ttgattccct ttcttcacat aaaaatatca 2250
 gaaattacat tttataactg cagtgggtata aatgcaaata tactattgtt 2300

acatgtgaaa aaatatttatt tgacttaaaa gtttatttat ttgttttttt 2350
 gctcctgatt ttaagacaat aagatgtttt catgggcccc taaaagtatc 2400
 atgagccttt ggcaactgcg ctgccaagcc tagtggagaa gtcaaccctg 2450
 agaccagggtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500
 acacaaatat gtcatatatc tttttttaaa aaaagtattt cattgaagca 2550
 agcaaaatga aagcattttt actgattttt aaaattggtg ctttagatat 2600
 atttgactac actgtattga agcaaataga ggaggcacia ctccagcacc 2650
 ctaatggaac cacatttttt tcaacttagct ttctgtgggc atgtgtaatt 2700
 gtattctctg cggtttttaa tctcacagta ctttatttct gtcttgtccc 2750
 tcaataatat cacaacaat attccagtca ttttaatggc tgcataataa 2800
 ctgatccaac aggtgttagg tgttctgggt tagtgtgagc actcaataaa 2850
 tattgaatga atgaacgaaa aaaaaaaaaa aaa 2883

<210> 24
 <211> 616
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-33
 <223> Signal peptide.

<220>
 <221> TRANSMEM
 <222> 13-40
 <223> Transmembrane domain (type II).

<400> 24
 Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu
 1 5 10 15
 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
 35 40 45
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
 50 55 60
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
 65 70 75
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
 80 85 90

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser
 95 100 105
 Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile
 110 115 120
 Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp
 125 130 135
 Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg
 140 145 150
 Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe
 155 160 165
 Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg
 170 175 180
 Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile
 185 190 195
 Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg
 200 205 210
 Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val
 215 220 225
 Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu
 230 235 240
 Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe
 245 250 255
 Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp
 260 265 270
 Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu
 275 280 285
 Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His
 290 295 300
 Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln
 305 310 315
 Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg
 320 325 330
 Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser
 335 340 345
 Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp
 350 355 360
 Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln
 365 370 375
 Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro

	380		385		390
Gln Asp Glu Arg	Lys 395	Ala Trp Arg Arg	Cys 400	Asp Arg Gly Gly	Phe 405
Trp Ala Asp Asp	Asp 410	Tyr Ser Arg Cys	Gln 415	Tyr Ala Asn Asp	Val 420
Thr Arg Val Leu	Tyr 425	Met Phe Asn Gln	Met 430	Pro Leu Asn Leu	Thr 435
Asn Ala Val Ala	Thr 440	Ala Arg Gln Leu	Leu 445	Ala Tyr Thr Val	Glu 450
Ala Ala Asn Phe	Ser 455	Asp Lys Met Asp	Val 460	Ile Phe Val Ala	Glu 465
Met Ile Glu Lys	Phe 470	Gly Arg Phe Thr	Lys 475	Glu Glu Lys Ser	Lys 480
Glu Leu Gly Asp	Val 485	Met Val Asp Ile	Ala 490	Ser Asn Ile Met	Leu 495
Ala Asp Glu Arg	Val 500	Leu Trp Leu Ala	Gln 505	Arg Glu Ala Lys	Ala 510
Cys Ser Arg Ile	Val 515	Gln Cys Leu Gln	Arg 520	Ile Ala Thr Tyr	Arg 525
Leu Ala Gly Gly	Ala 530	His Val Tyr Ser	Thr 535	Tyr Ser Pro Asn	Ile 540
Ala Leu Glu Ala	Tyr 545	Val Ile Lys Ser	Thr 550	Gly Phe Thr Gly	Met 555
Thr Cys Thr Val	Phe 560	Gln Lys Val Ala	Ala 565	Ser Asp Arg Thr	Gly 570
Leu Ser Asp Tyr	Gly 575	Arg Arg Asp Pro	Glu 580	Gly Asn Leu Asp	Lys 585
Gln Leu Ser Phe	Lys 590	Cys Asn Val Ser	Asn 595	Thr Phe Ser Ser	Leu 600
Ala Leu Lys Val	Cys 605	Tyr Ile Leu Gln	Ser 610	Phe Lys Thr Ile	Tyr 615

Ser

<210> 25
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24

<223> Synthetic construct

<400> 25

gaggactcac caatctggtt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

gcgtggggat gtctaggagc tcgaagggtg tgctgggcct ctcggtgctg 50

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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150

aaaaagaaaa cattcgtctt ttgggagaac agattatctt gactgagcaa 200

cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250

atgacttgaa tgtgaaatat ctgttgga gacaacacga gtttgtgtgt 300

gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350

actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400

ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450

tttggaagag tctgtctggg tgatcctggt agaagcccca ttagggtcac 500

tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

ggaagggatg gatagtagca tccacctgag tagtctgatc agtcggcatg 600
 atgacgaagc caccagaaca tcgacctcag aaggactgga ggaaggtgaa 650
 gtggagggag agacgctcct gatcgctcgaa tcc 683

<210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-21
 <223> Signal peptide.

B1
 <400> 29
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 20 25 30
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
 50 55 60
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
 65 70 75
 Lys Gly Ser Gln Lys Ser
 80

<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<400> 30
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 tccgtggatt cctctgctaa gaccgtgcc atgccagtga cggtaaccgc 150
 caccaccatc acaaccacca cgacgtcatc ttcgggcctg gggcccccca 200
 tgatcgtggg gtccccctcg gccctgacac agcccctggg tctccttcgc 250
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 gggcgcttg acgggggtcca tgggcaactg gtccatgttc acctggtgct 350
 tctgcttctc cgtgaccctg atcatcctca tcgtggagct gtgcgggctc 400
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ctatgcggcc ctcttctgcc tctcggcctc catcatctac cccaccacct 500
 atgtccagtt cctgtccac gccggttcgc gggaccacgc catcgccgcc 550
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<210> 31
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 31

Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr
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 35 40 45
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
 110 115 120
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 125 130 135
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
 140 145 150
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
 155 160 165
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
 170 175 180
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
 185 190 195
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
 200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu
 215 220 225

Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
 230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
 245 250 255

Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln
 260 265 270

Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr
 275 280 285

Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr
 290 295 300

Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
 305 310 315

His Leu Val Phe Val Lys Val
 320

<210> 32
 <211> 3680
 <212> DNA
 <213> Homo sapiens

<400> 32
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 ctggccagcc tatgcatttt taagaaatta ttctgtatta ggtgctgtgc 200
 taaacattgg gcactacagt gacccaaaaca gactgaattc cccaagagcc 250
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 ttattactca ctatgactaa gggtcacaaa tgggggtacgt tgatggagag 350
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 aggaaagctc ctctgacgag gtggtatttc agcccaaact ggaagaatga 450
 gaaagagcta gccagccatc agaatagtcc agaagagatg gggagcacta 500
 cactcactac actttggcct gagaaaatag catgggattg gaggaggctg 550
 ggggaacacc acttctgccg acctgggcag gaggcattga gggcttgaga 600
 aagggcaatg gcagtagcag tagaaaggac agggtaggag cagggacttt 650
 gcaggtggaa tcattaggtc ttatcaacag atatgggcaa gcaaagccag 700

gggagaattg atggtaatgc tgaggtttgg agccaggcta gatgggacag 750
 tgggtgggtga tgcaaaggaa agaggtcagg aagcagggcc agacgtgggg 800
 agaaggtgtg ggggttttgg ttccatcttg ccgagtctgc cggaatgtgg 850
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 agaagtcttg gatgccacac tcttcttctt tctctctctt ccctctctct 950
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B1

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 tgccacagag ctgggacttc atgttcttct agagagggcc acaagagggc 3250
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taatataaaa atctttgtaa atctctaaaa 3680

<210> 33
<211> 335
<212> PRT
<213> Homo sapiens

<400> 33

Met Phe Leu Ala Thr Leu Ser Phe Leu Leu Pro Phe Ala His Pro
1 5 10 15

Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser
20 25 30

Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
35 40 45

His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
50 55 60

Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
65 70 75

Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
80 85 90

Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
95 100 105

Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
110 115 120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
125 130 135

Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
140 145 150

Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
155 160 165

Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
170 175 180

Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
185 190 195

His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
200 205 210

Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
215 220 225

Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
230 235 240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
305 310 315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
320 325 330

Glu Pro Glu Glu Gln
335

<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct

<400> 34
tgtcctttgt cccagacttc tgtcc 25

<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 35
ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50

<210> 36
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 37
ggcgagccct aactatccag gag 23

B1
<210> 38
<211> 39
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-39
<223> Synthetic construct.

<400> 38
ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 39
ctgctgcaaa gcgagcctct tg 22

<210> 40
<211> 2084
<212> DNA
<213> Homo sapiens

<400> 40
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ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150
tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200
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caatctattc ttgccacatc aagggtattg tattccttta aaaaaaac 300

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gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450
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ttgggtgcct taaaaactca atgagaatca tggt 2084

<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

B1
<400> 41
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
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Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
110 115 120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu
 200 205 210
 Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn
 215 220 225
 Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe
 230 235 240
 Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu
 245 250 255
 Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser
 260 265 270
 His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu
 275 280 285
 Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser
 290 295 300
 Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu
 305 310 315
 Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu
 320 325 330
 Arg Thr Ser Val

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
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 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagaçgt ggaggccctc 150
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccacccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300
 tacaagtact tcatgcccac gagcaccatt taccgtggag agatgtgctt 350
 ttttgattct gaggatcctg caaattccct tcgtggagga gagcctaact 400
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
 atcattgatg tgccgtgcc cagtttctct gatagtgacc ctgcagcaat 500
 tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgcc ctcaatactt ctattgttat gcctccaaaa 600
 aatctggtag agctcttttg caaactggcg agtggcagat atctgcctca 650
 aacttatgtg gttcgagaag acctagtgc tgtggaggaa attcgtgatg 700
 ttagtaacct tggcatcttt atttaccac tttgcaataa cagaaagtcc 750
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 tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850
 ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900
 agaagtcaga gatttacaat atgacttta cattaagggt tatgggatac 950
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 ttctttgcat ttatagggt tagatttctg aaagcagcat gaatatatca 1150
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 tttttctttt cctttaagta agctctttat tcatcttatg gtggagcaat 1250
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 ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
 aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500
 tgtgtagggt ctgaatgctg taaggagttt aggttgatg aattctacaa 1550
 ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43
 <211> 263
 <212> PRT
 <213> Homo sapiens

<400> 43
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 Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
 20 25 30
 Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
 35 40 45
 Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50										55					60				
Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr					
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Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys					
				80					85					90					
Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu					
				95					100					105					
Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp					
				110					115					120					
Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp					
				125					130					135					
Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr					
				140					145					150					
Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu					
				155					160					165					
Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe					
				170					175					180					
Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val					
				185					190					195					
Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn					
				200					205					210					
Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe					
				215					220					225					
Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala					
				230					235					240					
Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile					
				245					250					255					
Val	Glu	Thr	Lys	Ile	Cys	Gln	Glu												
				260															

<210> 44
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 44
 gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgcagtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
ggaggagggga gggcgggcag ggcgcagccc agagcagccc cgggcaccag 50

cacggactct ctcttccagc ccaggtgccc cccactctcg ctccattcgg 100
 cgggagcacc cagtctctgta cgccaaggaa ctggctctgg gggcaccatg 150
 gtttcggcgg cagccccag cctcctcadc cttctgttgc tgctgctggg 200
 gtctgtgcct gctaccgacg cccgctctgt gccctgaag gccacgttcc 250
 tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggcctcctcc 300
 ccgagcctcc cgccaccctg gaccccgcc ctcagcccca catcgatggg 350
 gcccagccc acaaccctgg ggggcccadc acccccacc aacttcctgg 400
 atgggatagt ggacttcttc cgccagtacg tgatgctgat tgctgtggtg 450
 ggctccctgg cttttctgct gatgttcadc gtctgtgccg cggtcadcac 500
 ccggcagaag cagaaggcct cggcctatta cccatcgtcc ttccccaaga 550
 agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600
 gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650
 ctcccggcag ctccaggccg acatcttggc cgccaccag aacctcaagt 700
 ccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750
 ggcaggggcg cagaggaaga ggagaagggc agccaggagg gggaccagga 800
 agtccaggga catggggtcc cagtggagac accagaggcg caggaggagc 850
 cgtgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900
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 tccttcacct cagcagcccc aaagggtac atcctacagc acagctcccc 1250
 tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300
 cccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaac 1350
 tactttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400
 aatactgtc ttaattttcc tgaagggtggc cccctgttcc tagttggtcc 1450
 aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500

caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550
 gatcagggttg aatgaatgga actcttctctg tctggcctcc aaagcagcct 1600
 agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650
 ggggctgggg aagggtttct gacgcccagc ctggagcagg ggggccctgg 1700
 ccaccccctg ttgtctcacac attgtctggc agcctgtgtc cacaatattc 1750
 gtcagtcctc gacagggagc ctgggctccg tcctgcttta gggaggctct 1800
 ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850
 gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
 attccggcct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950
 aaaaaaaaaa aaaaaaaga 1969

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 50
 Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
 20 25 30
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
 35 40 45
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
 65 70 75
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
 80 85 90
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
 95 100 105
 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
 110 115 120
 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
 125 130 135
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
 140 145 150
 Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
 155 160 165

Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr
 170 175 180
 Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp
 185 190 195
 Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys
 200 205 210
 Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro
 215 220 225
 Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
 230 235 240
 Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly
 245 250 255
 Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro
 260 265 270
 Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val
 275 280

<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
 gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50
 gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100
 gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150
 agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200
 cctggcctgc ctctgtctgg ccctctgcct gggcagtggg gaggctggcc 250
 ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
 ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350
 caaagaggcc ggaggggcag ctggctctaa agtcagttag gcccttggcc 400
 aagggaccag agaagcagtt ggcaactggag tcaggcaggt tccaggcttt 450
 ggcgcagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500
 gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550
 acggagcaga tgctgtccgc ggctcctggc agggggtgcc tggccacagt 600
 ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg 650
 ccttgagggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750
 ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac 800
 caacactcag ggagctgtgg cccagcctgg ctatggttca gtgagagcca 850
 gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900
 ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtg 950
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
 gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050
 agtgggtgga gcagtggcaa cagtgggtggc agcagaggtg acagcggcag 1100
 tgagtccctc tggggatcca gcaccggctc ctctccggc aaccacggtg 1150
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 gaagcccggg ggagcgggga atctgggatt cagggttca gaggacaggg 1250
 agtttccagc aacatgaggg aaataagcaa agagggcaat cgcctccttg 1300
 gaggctctgg agacaattat cgggggcaag ggtcgagctg gggcagtgga 1350
 ggaggtgacg ctgttggtg agtcaatact gtgaactctg agacgtctcc 1400
 tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500
 ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550
 ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600
 aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 52
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 20 25 30
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
 35 40 45
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50 55 60
 Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr
 65 70 75
 Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly
 80 85 90
 Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala
 95 100 105
 Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val
 110 115 120
 Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val
 125 130 135
 Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile
 140 145 150
 Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro
 155 160 165
 Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser
 170 175 180
 Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln
 185 190 195
 Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly
 200 205 210
 Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln
 215 220 225
 Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly
 230 235 240
 Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser
 245 250 255
 Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly
 260 265 270
 Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser
 275 280 285
 Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser
 290 295 300
 Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly
 305 310 315
 Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His
 320 325 330
 Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly
 335 340 345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
 350 355 360
 Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
 365 370 375
 Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
 380 385 390
 Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
 395 400 405
 Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
 410 415 420
 Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
 425 430 435
 Ser Ser Arg Ile Pro
 440

<210> 53
 <211> 3580
 <212> DNA
 <213> Homo sapiens

<400> 53
 gaccggtccc tccggtcctg gatgtgcgga ctctgctgca gcgagggctg 50
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 ctttgctgac catgttggtc ccttgctgga atattaccgg gacatcttca 150
 ctctcctgct gcgcctgcac cggagcttgg tgttgctgca ggagagttag 200
 gggaagatgt gtttcctgaa caagctgctg ctacttgctg tcttgggctg 250
 gcttttccag attcccacag tccctgagga cttgttcttt ctggaagagg 300
 gtccctcata tgcctttgag gtggacacag tagccccaga gcatggcttg 350
 gacaatgcgc ctgtggtgga ccagcagctg ctctacacct gctgccccta 400
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 gacggagtgg gggcttcatg aggaaaatca cccccaccac taccaccagc 500
 ctgggagccc agccttccca gaccagccag gggctgcagg cacagctcgc 550
 ccaggccttt ttccacaacc agccgccttc cttgcgcgg accgtagagt 600
 tcgtggcaga aagaattgga tcaaactgtg taaacatat caaggctaca 650
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gagttctgtc aaaggaagag ccctggggct gtgcgggcgc tgcttccaga 850
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ttattagctg ggcatggtgg tgtgtgcctg taatcccagc tactcaggag 2300
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 ccaccaggca gggcgggctc ccgcgcgcgc cgccgccacc accgtccagg 3450
 ggccggtaga caaagtggaa gtcgcgcttg ggctcgctgc gcagcaggta 3500
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 cgtccaccag cacgaacagc cgggtgcgct 3580

<210> 54
 <211> 280
 <212> PRT
 <213> Homo sapiens

<400> 54

Met Cys Phe Leu Asn Lys Leu Leu Leu Leu Ala Val Leu Gly Trp
1 5 10 15
Leu Phe Gln Ile Pro Thr Val Pro Glu Asp Leu Phe Phe Leu Glu
20 25 30
Glu Gly Pro Ser Tyr Ala Phe Glu Val Asp Thr Val Ala Pro Glu
35 40 45
His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr
50 55 60
Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser
65 70 75
Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys
80 85 90
Ile Thr Pro Thr Thr Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln
95 100 105
Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His
110 115 120
Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu
125 130 135
Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val
140 145 150
Ala Asp Leu Val Arg Gln Ala Glu Ser Leu Leu Gln Glu Gln Leu
155 160 165
Val Thr Gln Gly Glu Glu Gly Gly Asp Pro Ala Gln Leu Leu Glu
170 175 180
Ile Leu Cys Ser Gln Leu Cys Pro His Gly Ala Gln Ala Leu Ala
185 190 195
Leu Gly Arg Glu Phe Cys Gln Arg Lys Ser Pro Gly Ala Val Arg
200 205 210
Ala Leu Leu Pro Glu Glu Thr Pro Ala Ala Val Leu Ser Ser Ala
215 220 225
Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp
230 235 240
Leu Ser Ala Asn Ile Thr Ala Leu Ile Arg Arg Glu Val Lys Ala
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Ala Val Ser Arg Thr Leu Arg Ala Gln Gly Pro Glu Pro Ala Ala
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Arg Gly Glu Arg Arg Gly Cys Ser Arg Ala
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<210> 55
<211> 2401
<212> DNA
<213> Homo sapiens

<400> 55
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a 2401

<210> 56
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 56
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 35 40 45
 Pro Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr Val Pro
 50 55 60
 Ile Leu Gly Asn Lys Thr Leu Pro Ser Arg Cys His Gln Cys Val
 65 70 75
 Ile Val Ser Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro
 80 85 90
 Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro
 95 100 105
 Thr Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg
 110 115 120
 Val Val Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln
 125 130 135
 Glu Phe Val Asn Arg Thr Pro Glu Thr Val Phe Ile Phe Trp Gly
 140 145 150
 Pro Pro Ser Lys Met Gln Lys Pro Gln Gly Ser Leu Val Arg Val
 155 160 165
 Ile Gln Arg Ala Gly Leu Val Phe Pro Asn Met Glu Ala Tyr Ala
 170 175 180
 Val Ser Pro Gly Arg Met Arg Gln Phe Asp Asp Leu Phe Arg Gly
 185 190 195
 Glu Thr Gly Lys Asp Arg Glu Lys Ser His Ser Trp Leu Ser Thr
 200 205 210
 Gly Trp Phe Thr Met Val Ile Ala Val Glu Leu Cys Asp His Val
 215 220 225
 His Val Tyr Gly Met Val Pro Pro Asn Tyr Cys Ser Gln Arg Pro
 230 235 240
 Arg Leu Gln Arg Met Pro Tyr His Tyr Tyr Glu Pro Lys Gly Pro
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 Asp Glu Cys Val Thr Tyr Ile Gln Asn Glu His Ser Arg Lys Gly
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<210> 57
 <211> 4277
 <212> DNA
 <213> Homo sapiens

<400> 57

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<210> 58
 <211> 1115

<212> PRT
<213> Homo sapiens

<400> 58

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Asp Leu Asn Glu Val Pro Gln Val Thr Val Gln Pro Ala Ser Thr
35 40 45
Val Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu
50 55 60
Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu
65 70 75
Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr
80 85 90
Leu Val Ile Thr Ala Leu Asn Asn His Thr Val Gly Arg Tyr Gln
95 100 105
Cys Val Ala Arg Met Pro Ala Gly Ala Val Ala Ser Val Pro Ala
110 115 120
Thr Val Thr Leu Ala Asn Leu Gln Asp Phe Lys Leu Asp Val Gln
125 130 135
His Val Ile Glu Val Asp Glu Gly Asn Thr Ala Val Ile Ala Cys
140 145 150
His Leu Pro Glu Ser His Pro Lys Ala Gln Val Arg Tyr Ser Val
155 160 165
Lys Gln Glu Trp Leu Glu Ala Ser Arg Gly Asn Tyr Leu Ile Met
170 175 180
Pro Ser Gly Asn Leu Gln Ile Val Asn Ala Ser Gln Glu Asp Glu
185 190 195
Gly Met Tyr Lys Cys Ala Ala Tyr Asn Pro Val Thr Gln Glu Val
200 205 210
Lys Thr Ser Gly Ser Ser Asp Arg Leu Arg Val Arg Arg Ser Thr
215 220 225
Ala Glu Ala Ala Arg Ile Ile Tyr Pro Pro Glu Ala Gln Thr Ile
230 235 240
Ile Val Thr Lys Gly Gln Ser Leu Ile Leu Glu Cys Val Ala Ser
245 250 255
Gly Ile Pro Pro Pro Arg Val Thr Trp Ala Lys Asp Gly Ser Ser
260 265 270

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu
 275 280 285
 Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met
 290 295 300
 Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr
 305 310 315
 Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser
 320 325 330
 Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu
 335 340 345
 Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala
 350 355 360
 Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala
 365 370 375
 Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln
 380 385 390
 Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln
 395 400 405
 Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp
 410 415 420
 Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu
 425 430 435
 Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg
 440 445 450
 Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu
 455 460 465
 Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser
 470 475 480
 Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro
 485 490 495
 Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val
 500 505 510
 Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile
 515 520 525
 Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu
 530 535 540
 Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys
 545 550 555
 Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg

560 565 570
 Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln
 575 580 585
 Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp
 590 595 600
 His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile
 605 610 615
 Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg
 620 625 630
 Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys
 635 640 645
 Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile
 650 655 660
 Pro Pro Ser Arg Leu Ser Val Glu Ile Thr Gly Leu Glu Lys Gly
 665 670 675
 Thr Ser Tyr Lys Phe Arg Val Arg Ala Leu Asn Met Leu Gly Glu
 680 685 690
 Ser Glu Pro Ser Ala Pro Ser Arg Pro Tyr Val Val Ser Gly Tyr
 695 700 705
 Ser Gly Arg Val Tyr Glu Arg Pro Val Ala Gly Pro Tyr Ile Thr
 710 715 720
 Phe Thr Asp Ala Val Asn Glu Thr Thr Ile Met Leu Lys Trp Met
 725 730 735
 Tyr Ile Pro Ala Ser Asn Asn Asn Thr Pro Ile His Gly Phe Tyr
 740 745 750
 Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr Lys
 755 760 765
 Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His
 770 775 780
 Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn
 785 790 795
 Glu Gly Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr
 800 805 810
 Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro
 815 820 825
 Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr Ile Glu Arg
 830 835 840
 Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp Leu Pro
 845 850 855

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile
 860 865 870
 Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
 875 880 885
 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro
 890 895 900
 Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His
 905 910 915
 Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala
 920 925 930
 Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala
 935 940 945
 Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu
 950 955 960
 Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His
 965 970 975
 Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly
 980 985 990
 Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro
 995 1000 1005
 Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys
 1010 1015 1020
 Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg
 1025 1030 1035
 Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro
 1040 1045 1050
 Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu
 1055 1060 1065
 Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp
 1070 1075 1080
 Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly
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 Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr
 1100 1105 1110
 Pro Pro Leu Thr Ile
 1115

<210> 59
 <211> 25
 <212> DNA
 <213> Artificial

<220>
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<222> 1-25
<223> Synthetic construct.

<400> 59
gggaaacaca gcagtcattg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 60
gcacacgtag cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

<400> 61
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<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

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<223> unknown base

<400> 62
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 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
 cacatggaaa a 1661

<210> 63
 <211> 487
 <212> PRT
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

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 1 5 10 15
 Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Arg
 20 25 30
 Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala
 35 40 45
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val
 50 55 60
 Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr Thr Pro Gly Thr Pro
 65 70 75
 Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser
 80 85 90
 Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg
 95 100 105
 Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg Asn Phe
 110 115 120
 Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val
 125 130 135
 Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp
 140 145 150
 Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His
 155 160 165
 Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala
 170 175 180
 Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val
 185 190 195
 Xaa Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser
 200 205 210
 Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys
 215 220 225
 Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His Met
 230 235 240
 Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val
 245 250 255
 Glu Glu Leu Asn Arg Leu Gly Met Met Ile Asp Leu Ser Tyr Ala

260 265 270
 Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro
 275 280 285
 Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu
 290 295 300
 Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly
 305 310 315
 Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu
 320 325 330
 Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg
 335 340 345
 Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp
 350 355 360
 Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr
 365 370 375
 Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu
 380 385 390
 Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg
 395 400 405
 Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val
 410 415 420
 Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser
 425 430 435
 His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val
 440 445 450
 Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala
 455 460 465
 Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro
 470 475 480
 Thr Phe Thr Gln Trp Leu Cys
 485

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 65
gtcacacaca gctctggcag ctgag 25

<210> 66
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 66
ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67
<211> 1564
<212> DNA
<213> Homo sapiens

<400> 67
tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50
aacacccaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100
ggcccagcaa gcctgataag catgaagctc ttatcttttg tggctgtggt 150
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
gcccattgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400
atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450
gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcggaag acagtcttcg 650
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ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800
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gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950
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cagctctgag tcttgggaat gttgttacct ttggaagata aagctgggtc 1050
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ttttatttct ctca 1564

<210> 68
<211> 183
<212> PRT
<213> Homo sapiens

<400> 68
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
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Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
20 25 30
Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
35 40 45
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
50 55 60

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
 65 70 75
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
 80 85 90
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
 95 100 105
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
 110 115 120
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
 125 130 135
 Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
 140 145 150
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
 155 160 165
 Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
 170 175 180
 Met Leu Ser

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
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 tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggctctccc 150
 tccctttgca ttcccacccc tccgggcttt gcgtcttctt ggggaccccc 200
 tcgcccggag atggccgcgt tgatgcggag caaggattcg tctgctgcc 250
 tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300
 tcgcgggcca aactcaactc catcaagtcc tctctgggcg gggagacgcc 350
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400
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 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550
 gcatgtgtg cccagtagc cgctgcaata atggcatctg tatccagtt 600
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cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700
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 gacccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg 800
 tcatttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850
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 ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050
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 gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150
 aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200
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 aaaatactcc tagaataact tgttatacaa taggttctaa aaataaaatt 1450
 gctaaacaag aaatgaaaac atggagcatt gttaatttac aacagaaaat 1500
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 cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650
 ccacaaatac ttttttttca aaattttagt ttacctgta attaataaga 1700
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 atataacaat tattatattt acaatttggt ttctgcaata tttttcttat 2950
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 ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050
 gcagaatata ttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100
 taagataaaa tctattaaat ttttctcctc taaaaactga aaaaaaaaaa 3150
 aaaaaaaaaa aaaaaaaaaa 3170

<210> 70
 <211> 259
 <212> PRT
 <213> Homo sapiens

<400> 70
 Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu
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 Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser
 20 25 30
 Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
 35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
 50 55 60
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
 65 70 75
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
 80 85 90
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
 95 100 105
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
 110 115 120
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
 125 130 135
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
 140 145 150
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
 155 160 165
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
 170 175 180
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
 185 190 195
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
 200 205 210
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
 215 220 225
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 230 235 240
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
 245 250 255
 Cys Gln Lys Ile

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

<400> 71
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 tggcctccca aagtgttggg attacaggcg tgagccaccg cgcccggcca 100
 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250
 atatatttagt aattcatatg ttttagatta taggttttaa catacttgtg 300
 aaaataacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350
 ggatttgttc ttttatcccc cttttaaaagt catccgtcct tggctcagga 400
 tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450
 tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500
 gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550
 ctcaagcccc caacatccca gtcctcagtc ctcagtcac ttgacttcaa 600
 atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650
 agcaccagag ccaggcagtc actgttctc ctcttggtt ggagtccttt 700
 ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750
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 tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850
 atacccccag ctcttaagat cccagcttct gcagtggaaa tgcctggttc 900
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 aatcagattc ccatacagctt gtattcgaag tctttaagtg agcctttgaa 1050
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 ccgtcattac ctctgcagc ctgacaagct catcactgaa ttctgctagt 1150
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 gatagctcac gtgatgtgga aaacaccagt tggatcaatgg ctcatcgtt 1400
 aaaaagcagc ccttttgctt ttttgtttt ggaccagggtg ttggctgtgg 1450
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 ttcttctgcc ctaatcagac tgcaccacaa gtgcagcata cagtatgcat 1550
 tttaaagatg cttgggcccag gcgggggtgg tgatgccat aatcccagtg 1600
 ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700
gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750
gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800
ctgaaaaga 1809

<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72

Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile
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Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
20 25 30
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
35 40 45
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
50 55 60
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
65 70 75
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys
 230 235 240
 Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala
 245 250 255
 Val Gln Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser
 260 265 270
 Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser
 275 280 285
 Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln
 290 295 300
 Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn
 305 310 315
 Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr
 320 325 330
 Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg
 335 340 345
 Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp
 350 355 360

Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 73
 aattcatggc aaatatttcc cttccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 74
 tggtaaactg gcccaaactc gg 22

<210> 75
 <211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcac ccgtccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

B1
<400> 76
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ccgaatcctg ctttggaac ttgtgcttct gcagagctct gctgttctcc 100
tgactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggagggt 200
caccgacggc cccccggcca cccccgccta ctgggacggc gagaaggagg 250
tgctggcggt ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300
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aactgcaa at agggaggccc tgggctcctg gctggggccag cagctgcacc 1100
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<210> 77
<211> 341
<212> PRT
<213> Homo sapiens

<400> 77
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Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
20 25 30
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
 80 85 90
 Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
 95 100 105
 Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg
 110 115 120
 Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro
 125 130 135
 Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu
 140 145 150
 Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp
 155 160 165
 Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu
 170 175 180
 His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala
 185 190 195
 Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser
 200 205 210
 Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val
 215 220 225
 Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln
 230 235 240
 Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu
 245 250 255
 Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu
 260 265 270
 Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn
 275 280 285
 Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg
 290 295 300
 Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
 305 310 315
 Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp
 320 325 330
 Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys
 335 340

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 78

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<210> 79
<211> 475
<212> PRT
<213> Homo sapiens

<400> 79
Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
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Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
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Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
35 40 45
Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
50 55 60
Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
65 70 75
Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
80 85 90
Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
95 100 105

Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val
 110 115 120
 Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val
 125 130 135
 Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr
 140 145 150
 Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe
 155 160 165
 Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr
 170 175 180
 Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met
 185 190 195
 Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr
 200 205 210
 Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp
 215 220 225
 Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe
 230 235 240
 Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu
 245 250 255
 Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe
 260 265 270
 Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser
 275 280 285
 Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro
 290 295 300
 Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val
 305 310 315
 Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile
 320 325 330
 Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe
 335 340 345
 Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu
 350 355 360
 Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn
 365 370 375
 Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile
 380 385 390
 Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys

395 400 405
 Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser
 410 415 420
 Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu
 425 430 435
 Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly
 440 445 450
 Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser
 455 460 465
 Ala Cys Ser Thr Leu Leu Val His Leu Ile
 470 475

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 80
 ttttgcggtc accattgtct gc 22

<210> 81
 <211> 23
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Artificial sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 81
 cgtaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 82
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83
 <211> 1844

<212> DNA
<213> Homo sapiens

<400> 83

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aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200
ctatgagcag ctgctcaagg tggcgcctg gggcgcctc cggaccctga 250
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cacaagctct gccagggcct gggcgcctc ctgaccaagt tcaccagta 500
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 ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750
 aaaacacgac ccacacgagg acctcgcatt aaagtatttt cggaaaaaaaa 1800
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 84
 Met Ala Pro Leu Ala Leu His Leu Leu Val Leu Val Pro Ile Leu
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 20 25 30
 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
 35 40 45
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
 50 55 60
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
 80 85 90
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
 125 130 135
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
 140 145 150
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
 155 160 165

Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
 170 175 180
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
 185 190 195
 Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr
 200 205 210
 Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala
 215 220 225
 Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr
 230 235 240
 Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp
 245 250 255
 Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro
 260 265 270
 Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala
 275 280 285
 Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln
 290 295 300
 Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala
 305 310 315
 Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile
 320 325 330
 Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg
 335 340 345
 Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg
 350 355 360
 Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn
 365 370 375
 Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu
 380 385 390
 Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala
 395 400 405
 Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu
 410 415 420
 Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp
 425 430 435
 Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser
 440 445 450
 Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu

455 460 465
 Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly
 470 475 480
 Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys
 485 490 495
 Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro
 500 505 510
 Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu
 515 520 525
 Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp
 530 535 540
 Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu
 545 550 555
 Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His
 560 565

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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 ctctgggccc gccttctgcc tgcattggacg ctctgaagcc accctgtctc 100
 tggaggaacc acgagcggag gaagaaggac agggactcgt gtggcaggaa 150
 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200
 cccctcga gggctgaat ttctgtctgc tgttcacaaa gatgcttttt 250
 atctttaact ttttgttttc cccacttcgg accccggcgt tgatctgcat 300
 cctgacattt ggagctgcca tcttcttggt gctgatcacc agacctcaac 350
 ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggga 400
 ggagcacgga aggggggttt ccagaagaac aatgacctaa caagttgctg 450
 cttctcagat gccaaagacta tgtatgaggt tttccaaaga ggactcgtg 500
 tgtctgacaa tgggccctgc ttgggatata gaaaaccaa ccagccctac 550
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 ctgtctcttg cataaagggt ataatcatc accagaccag tttgtcggca 650
 tctttgctca gaataggcca gaggatga tctccgaatt ggcttggtac 700
 acgtactcta tggtagctgt acctctgtat gacaccttg gaccagaagc 750

catcgtacat attgtcaaca aggctgatat cgccatggtg atctgtgaca 800
 caccaccaaaa ggcatggtg ctgatagga atgtagagaa aggcttcacc 850
 ccgagcctga aggtgatcat ccttatggac ccctttgatg atgacctgaa 900
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 aaaagggat catcaggcat gatagtttct gggacaagct catctttgca 1450
 aagatccagg acagcctggg cggaagggtt cgtgtaattg tcaactggagc 1500
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 aatttttgta cagggggaga gcttacggtc atccttagta ggagtgggtg 2000
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 acaggcaagc aagatgcca cacaacaggc ttattttctg tgaaggaacc 3200
 aactgatctc cccaccctt ggattagagt tctgtctcta ccttaccac 3250
 agataacaca tggtgtttct acttgtaaatt gtaaagtctt taaaataaac 3300
 tattacagat aaaaaa 3316

<210> 86
 <211> 739
 <212> PRT
 <213> Homo sapiens

<400> 86
 Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg
 1 5 10 15
 Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
 20 25 30

Gly Ser Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser
 35 40 45
 Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile
 50 55 60
 Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys
 65 70 75
 Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg
 80 85 90
 Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val
 95 100 105
 Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn
 110 115 120
 Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu
 125 130 135
 Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu
 140 145 150
 Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys
 155 160 165
 Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His
 170 175 180
 Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala
 185 190 195
 Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr
 200 205 210
 Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu
 215 220 225
 Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile
 230 235 240
 Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu
 245 250 255
 Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro
 260 265 270
 Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu
 275 280 285
 Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe
 290 295 300
 Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys
 305 310 315
 Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr

320 325 330
 His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val
 335 340 345
 Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr
 350 355 360
 Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val
 365 370 375
 Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg
 380 385 390
 Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro
 395 400 405
 Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn
 410 415 420
 Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val
 425 430 435
 Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp
 440 445 450
 Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu
 455 460 465
 Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser
 470 475 480
 Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val
 485 490 495
 Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe
 500 505 510
 Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu
 515 520 525
 Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr
 530 535 540
 Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn
 545 550 555
 Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala
 560 565 570
 Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp
 575 580 585
 Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile
 590 595 600
 Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu
 605 610 615

Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His
 620 625 630
 Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp
 635 640 645
 Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly
 650 655 660
 Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile
 665 670 675
 Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr
 680 685 690
 Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser
 695 700 705
 Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly
 710 715 720
 Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu
 725 730 735
 His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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 cccctcatca agcccttttg ggctcggaag aagcggagct ggtaccttac 200
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 atcctggaca ctgcgcgagc catcagtga gccaatgaag acccagagcc 350
 agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgca 400
 gaggcagtgg tccccggcgg gtccctggacg tagaggtgta ttcaagtcgc 450
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 ccgggagcag ggccggggca tccatgtcat tgtcctcaac caggccacgg 550
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 ttctggaaga ggacctggac attgctgtgg attttttcag tttcctgagc 1350
 caatccatcc acctactgga ggaggatgac agcctgtact gcatctctgc 1400
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 cttagacact ggaccaggcc tcctctcagc cttctctttg tccagatttc 2650
 caaagctgga taagttggct attgattaaa aaaggagaag ccctctggga 2700
 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
 Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala
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 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
 110 115 120
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
 125 130 135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp
 140 145 150
 Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn
 155 160 165
 Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu
 170 175 180
 Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser
 185 190 195
 Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp
 200 205 210
 Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His
 215 220 225
 Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu
 230 235 240
 Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His
 245 250 255
 Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser
 260 265 270
 Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr
 275 280 285
 Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu
 290 295 300
 Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu
 305 310 315
 Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro
 320 325 330
 Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met
 335 340 345
 Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro
 350 355 360
 Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser
 365 370 375
 Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val
 380 385 390
 Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe
 395 400 405
 Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr
 410 415 420
 Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu

	425		430		435
Asp Pro Ala Leu	Leu Tyr Arg Val Glu	Thr Met Pro Gly Leu	Gly		
	440		445		450
Trp Val Leu Arg	Arg Ser Leu Tyr Lys	Glu Glu Leu Glu Pro	Lys		
	455		460		465
Trp Pro Thr Pro	Glu Lys Leu Trp Asp	Trp Asp Met Trp Met	Arg		
	470		475		480
Met Pro Glu Gln	Arg Arg Gly Arg Glu	Cys Ile Ile Pro Asp	Val		
	485		490		495
Ser Arg Ser Tyr	His Phe Gly Ile Val	Gly Leu Asn Met Asn	Gly		
	500		505		510
Tyr Phe His Glu	Ala Tyr Phe Lys Lys	His Lys Phe Asn Thr	Val		
	515		520		525
Pro Gly Val Gln	Leu Arg Asn Val Asp	Ser Leu Lys Lys Glu	Ala		
	530		535		540
Tyr Glu Val Glu	Val His Arg Leu Leu	Ser Glu Ala Glu Val	Leu		
	545		550		555
Asp His Ser Lys	Asn Pro Cys Glu Asp	Ser Phe Leu Pro Asp	Thr		
	560		565		570
Glu Gly His Thr	Tyr Val Ala Phe Ile	Arg Met Glu Lys Asp	Asp		
	575		580		585
Asp Phe Thr Thr	Trp Thr Gln Leu Ala	Lys Cys Leu His Ile	Trp		
	590		595		600
Asp Leu Asp Val	Arg Gly Asn His Arg	Gly Leu Trp Arg Leu	Phe		
	605		610		615
Arg Lys Lys Asn	His Phe Leu Val Val	Gly Val Pro Ala Ser	Pro		
	620		625		630
Tyr Ser Val Lys	Lys Pro Pro Ser Val	Thr Pro Ile Phe Leu	Glu		
	635		640		645
Pro Pro Pro Lys	Glu Glu Gly Ala Pro	Gly Ala Pro Glu Gln	Thr		
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<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

gatggcaaaa cgtgtgtttg acacg 25

<210> 90
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

β1 <400> 90
cctcaaccag gccacgggcc ac 22

<210> 91
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 91
cccaggcaga gatgcagtag aggc 24

<210> 92
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 92
cctccagtag gtggatggat tggctc 26

<210> 93
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 93
ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

<400> 94

B1
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actggaaatt tgttgtctag tgggtgtggg tgaataaagg agggcagaat 150
ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 200
gttacgtggc cggaatcatt cccttggctg ttaatttctc agaggaacga 250
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aaagcagcag aaaaatcagt tgtccatgaa catgagcaca gccacgacca 450
cacacagctg catgcctata ttggtgtttc cctcgttctg ggcttcgttt 500
tcatgttgct ggtggaccag attggttaact cccatgtgca ttctactgac 550
gatccagaag cagcaaggtc tagcaattcc aaaatcacca ccacgctggg 600
tctggttgct catgctgcag ctgatggtgt tgctttggga gcagcagcat 650
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cgggacattt ctttatgttg ccacagtaca tgtcctccct gaggtgggag 950
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 gaaagtagca caaataggat acagttgtat gtagtcattg gcaacaattg 2850
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B1

ttccttgatt ggatgttaac agctgactgg tgtgagactt gaggtttcat 2950
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<210> 95
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 95

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 Val Gly Cys Tyr Val Ala Gly Ile Ile Pro Leu Ala Val Asn Phe
 20 25 30
 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
 35 40 45
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
 215 220 225
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu		
245	250	255
Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly		
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg		
275	280	285
Leu Glu Val Ala Ala Leu Val Leu Gly Cys Leu Ile Pro Leu Ile		
290	295	300
Leu Ser Val Gly His Gln His		
305		

B1
 <210> 96
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 96
 gttgtgggtg aataaaggag ggcag 25

<210> 97
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 97
 ctgtgctcat gttcatggac aactg 25

<210> 98
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 98
 ggatgatttc atctocatta gcctgctgtc tctggctatg ttggtgggat 50

<210> 99
 <211> 1429

<212> DNA
<213> Homo sapiens

<400> 99

B1
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ctgattttga gatgatgggc ttgggaaacg ggcgtcgag catgaagtcg 150
ccgccccctg tgctggccgc cctggtggcc tgcattcatg tcttgggctt 200
caactactgg attgagagct cccggagcgt ggacctccag acacggatca 250
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gagaggctca tccgagtgtc gcaagaccag ttaaagacct tgcagaggaa 500
ttacggcagg ctgcagcagg atgtcctcca gtttcagaag aaccagacca 550
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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe
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Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg
35 40 45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg
50 55 60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
65 70 75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe
80 85 90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
95 100 105

Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
110 115 120

Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
155 160 165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
170 175 180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
185 190 195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
200 205 210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
215 220 225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser
230 235 240

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr
 245 250 255
 Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu
 260 265 270
 Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val
 275 280 285
 Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro
 290 295 300
 Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met
 305 310 315
 Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu
 320 325 330
 Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu
 335 340 345
 Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser
 350 355 360
 Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile
 365 370 375
 Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu
 380 385 390
 Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu
 395 400

<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

<400> 101
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 ttctacgctg gcattgccct cttcaccagt ggcttcctgc tcacccgttt 100
 ggagctcacc aaccatagca gctgccaaaga gccccaggc cctgggtccc 150
 tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccga 200
 ttttcgcggg ttgtgttggt gctgatagat gctctgcgat ttgacttcgc 250
 ccagccccag cattcacacg tgcctagaga gcctcctgtc tccctaccct 300
 tcctgggcaa actaagctcc ttgcagagga tcctggagat tcagccccac 350
 catgcccggc tctaccgatc tcaggttgac cctcctacca ccaccatgca 400
 ggcctcaag gccctcacca ctggctcact gcctaccttt attgatgctg 450
 gtagtaactt cgccagccac gccatagtgg aagacaatct cattaagcag 500

ctcaccagtg caggaaggcg tgtagtcttc atgggagatg atacctggaa 550
 agaccttttc cctggtgctt tctccaaagc tttcttcttc ccatccttca 600
 atgtcagaga cctagacaca gtggacaatg gcatcctgga acacctctac 650
 cccaccatgg acagtgggtga atgggacgtg ctgattgctc acttcctggg 700
 tgtggaccac tgtggccaca agcatggccc tcaccaccct gaaatggcca 750
 agaaacttag ccagatggac caggtgatcc agggacttgt ggagcgtctg 800
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 tggagaccat ggaggggaca gtgagctgga ggtctcagct gctctctttc 900
 tgtatagccc cacagcagtc ttccccagca ccccaccaga ggagccagag 950
 gtgattcctc aagttagcct tgtgccacg ctggccctgc tgctgggcct 1000
 gcccatccca tttgggaata tcggggaagt gatggctgag ctattctcag 1050
 ggggtgagga ctcccagccc cactcctctg ctttagccca agcctcagct 1100
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 gggagctcgg gccatgtgca tcgagtcttg ggctcgtttc tctctggtec 1350
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 gctagctggg ctttttcac gttgccctga agagacacct gtttgccact 1950

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 aatttatggt atggagcttg tgtggcggcg ctggtggccc tgtagctgc 2050
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 agtgaataa aatgataata t 3671

<210> 102
 <211> 1089
 <212> PRT
 <213> Homo sapiens

<400> 102

Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe
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 Leu Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu
 20 25 30
 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro
 35 40 45
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala
 50 55 60
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
 65 70 75
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val
 80 85 90
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
 95 100 105
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
 110 115 120
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
 125 130 135
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
 140 145 150
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys
 155 160 165
 Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp
 170 175 180
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe
 185 190 195
 Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

200 205 210
 Ile Leu Glu His Leu Tyr Pro Thr Met Asp Ser Gly Glu Trp Asp
 215 220 225
 Val Leu Ile Ala His Phe Leu Gly Val Asp His Cys Gly His Lys
 230 235 240
 His Gly Pro His His Pro Glu Met Ala Lys Lys Leu Ser Gln Met
 245 250 255
 Asp Gln Val Ile Gln Gly Leu Val Glu Arg Leu Glu Asn Asp Thr
 260 265 270
 Leu Leu Val Val Ala Gly Asp His Gly Met Thr Thr Asn Gly Asp
 275 280 285
 His Gly Gly Asp Ser Glu Leu Glu Val Ser Ala Ala Leu Phe Leu
 290 295 300
 Tyr Ser Pro Thr Ala Val Phe Pro Ser Thr Pro Pro Glu Glu Pro
 305 310 315
 Glu Val Ile Pro Gln Val Ser Leu Val Pro Thr Leu Ala Leu Leu
 320 325 330
 Leu Gly Leu Pro Ile Pro Phe Gly Asn Ile Gly Glu Val Met Ala
 335 340 345
 Glu Leu Phe Ser Gly Gly Glu Asp Ser Gln Pro His Ser Ser Ala
 350 355 360
 Leu Ala Gln Ala Ser Ala Leu His Leu Asn Ala Gln Gln Val Ser
 365 370 375
 Arg Phe Leu His Thr Tyr Ser Ala Ala Thr Gln Asp Leu Gln Ala
 380 385 390
 Lys Glu Leu His Gln Leu Gln Asn Leu Phe Ser Lys Ala Ser Ala
 395 400 405
 Asp Tyr Gln Trp Leu Leu Gln Ser Pro Lys Gly Ala Glu Ala Thr
 410 415 420
 Leu Pro Thr Val Ile Ala Glu Leu Gln Gln Phe Leu Arg Gly Ala
 425 430 435
 Arg Ala Met Cys Ile Glu Ser Trp Ala Arg Phe Ser Leu Val Arg
 440 445 450
 Met Ala Gly Gly Thr Ala Leu Leu Ala Ala Ser Cys Phe Ile Cys
 455 460 465
 Leu Leu Ala Ser Gln Trp Ala Ile Ser Pro Gly Phe Pro Phe Cys
 470 475 480
 Pro Leu Leu Leu Thr Pro Val Ala Trp Gly Leu Val Gly Ala Ile
 485 490 495

Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu
500 505 510

Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe
515 520 525

Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala
530 535 540

Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Phe
545 550 555

Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala
560 565 570

Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val
575 580 585

Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu
590 595 600

Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg
605 610 615

His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu
620 625 630

Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr
635 640 645

Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met
650 655 660

Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala
665 670 675

Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg
680 685 690

Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg
695 700 705

Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala
710 715 720

Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu
725 730 735

Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu
740 745 750

Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val
755 760 765

Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu
770 775 780

Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr

B1

	785		790		795
Val Val Pro Gln Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly	800		805		810
Arg Leu Glu Arg Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala	815		820		825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu	830		835		840
Thr Leu Leu Ala Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile	845		850		855
Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu	860		865		870
His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe	875		880		885
Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr	890		895		900
Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile	905		910		915
His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser	920		925		930
Cys Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala	935		940		945
Ser His Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp	950		955		960
Pro Phe Leu Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro	965		970		975
Pro Gly Asn Glu Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu	980		985		990
Glu Pro Leu Met Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe	995		1000		1005
Tyr Ala Ala Leu Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu	1010		1015		1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg	1025		1030		1035
Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe	1040		1045		1050
Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly	1055		1060		1065
Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe	1070		1075		1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

B1
<400> 103
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gcagttccct gtgtctctgg tggtttgctt aaacctgcaa acatcacctt 100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatacaac agaacgtggc cccagtgtgt gaccaaccac acgctgggtc 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
aaaaaatcgt gattaacttt atcacccctc atatctcgga tgattctaaa 750
atctctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagccca gcgggaacct gaggccccct caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900
gactctgaag aaaacacgga aggtacttct ctcaccagc aagagtcctt 950
cagcagaaca ataccctcgg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcggt 1100
ggcagtcctt ggcccgcaaa cgttacagta ctatacacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggagggggccg 1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggtgcg 1300
 agccttctga ggggatggg ctcgagagg agggcttct atctagactc 1350
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 catgcaattc atggaggaat gggggttata tgtgcagatg gaaaactgat 1450
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 cgtgtgtgat tggttcatgc atgtaggtct cttacaatg atgggtgggc 1650
 tctggagtcc aggggtggc cggtgttct atgcagagaa agcagtcatt 1700
 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104
 <211> 442
 <212> PRT
 <213> Homo sapiens

<400> 104
 Met Ser Tyr Asn Gly Leu His Gln Arg Val Phe Lys Glu Leu Lys
 1 5 10 15
 Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu
 20 25 30
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
 35 40 45
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
 50 55 60
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
 65 70 75
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
 80 85 90
 Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
 95 100 105
 His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
 110 115 120
 Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
 125 130 135
 Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
 140 145 150
 Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
 155 160 165

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile
 170 175 180
 Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys
 185 190 195
 Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys
 200 205 210
 Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val
 215 220 225
 Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro
 230 235 240
 Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu
 245 250 255
 Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser
 260 265 270
 Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys
 275 280 285
 Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys
 290 295 300
 Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser
 305 310 315
 Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu
 320 325 330
 Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp
 335 340 345
 Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro
 350 355 360
 Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr
 365 370 375
 Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
 380 385 390
 Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
 395 400 405
 Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
 410 415 420
 Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly
 425 430 435
 Leu Tyr Val Gln Met Glu Asn
 440

<210> 105

<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

B1
<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgccca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctcctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-51
<223> Synthetic construct.

<400> 109
ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacaat 50

c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

B1
<400> 110
cggacgcgtg ggccggacgcg tgggaggacg cgtgggtctc tgcggggaga 50
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100
tctgtgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150
gctcctgggg ggcccagatc atcggggggcc acgaggtgac cccccactcc 200
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cccaggaga agccgcctga gccacaacct tgcggcatgc aatgagatg 950
gccgtccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000
tggtcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val
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Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp
20 25 30

Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
35 40 45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
50 55 60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
65 70 75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
80 85 90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
95 100 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
110 115 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
125 130 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
140 145 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
155 160 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
170 175 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
185 190 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg
200 205 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg
215 220 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly
230 235 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 112
gacgtctgca acagctcctg gaag 24

B1
<210> 113
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 113
cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 114
tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50
cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100
cgctgtcggc gctgggcaag gtagcaggcg ccgccgtgct gctcaaggac 150
tatgtcaccg gtggggcttg ccccagcaag gccaccatcc ctgggaagac 200

ggtcatcgtg acggggcgcca acacaggcat cgggaagcag accgccttgg 250
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
 tgtcaacgcc cggcacctgg acttggcttc cctcaagtct atccgagagt 400
 ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450
 aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500
 gatgcagttt ggcgttaacc acctgggtca ctttctcttg aaaaacttgc 550
 tgctggacaa gctgaaagcc tcagccccct cgcgatcat caacctctcg 600
 tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650
 gaggaggaag tataacacca aagccgccta ctgccagagc aagctcgcca 700
 tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtgtg 750
 actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tgggcagaca 800
 cacgggcatc catggctcca ccttctccag caccacactc gggcccatct 850
 tctggctgct ggtcaagagc cccgagctgg ccgcccagcc cagcacatac 900
 ctggccgtgg cggaggaact ggcggatgtt tccggaaagt acttcgatgg 950
 actcaaacag aaggccccgg ccccgaggc tgaggatgag gaggtggccc 1000
 ggaggctttg ggctgaaagt gcccgcctgg tgggcttaga ggctccctct 1050
 gtgagggagc agcccctccc cagataacct ctggagcaga tttgaaagcc 1100
 aggatggcgc ctccagaccg aggacagctg tccgccatgc ccgagcttc 1150
 ctggcactac ctgagccggg agaccagga ctggcggccg ccatgcccgc 1200
 agtaggttct agggggcggt gctggccgca gtggactggc ctgcaggtga 1250
 gcactgcccc gggctctggc tggttccgtc tgctctgctg ccagcagggg 1300
 agaggggcca tctgatgctt cccctgggaa tctaaactgg gaatggccga 1350
 ggaggaaggg gctctgtgca cttgcaggcc acgtcaggag agccagcggg 1400
 gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450
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 gtcctctctg agccttgggt tcttcagcag tgagatgctc agaataactg 1550
 ctgtctccca tgatggtgtg gtacagcgag ctgttgtctg gctatggcat 1600
 ggctgtgccg ggggtgtttg ctgagggctt cctgtgccag agcccagcca 1650

gagagcaggt gcaggtgtca tcccagattc aggctctgca cggcatggag 1700
 tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750
 caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800
 gctcattt 1808

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116

Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
 1 5 10 15
 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
 20 25 30
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750
 cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850
 cccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900
 acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950
 cagccactc tctaccagat ccctagcctc tactgttct atgagaccaa 1000
 ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050
 tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100
 cagaaaatta gagaacttgc agaaccatgg ctacagaggc cagtgggtggc 1150
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200
 ggctgaagga cactgttgac ccaaaactgg tgaccctcaa ccaccgcatt 1250
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400
 gcaacattta tgatctatct gagctcggtg gaagctggag gagccacagc 1450
 cttcatctat gccaacctca gcgtgcctgt ggtaggaat gcagcactgt 1500
 tttggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550
 gctggctgtc ctgtcctggt gggagataag tgggtggcca acaagtggat 1600
 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650
 actgaactgt tggcagagag aagctgggtg agtcctgtgg ctttccagag 1700
 aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750
 ctggaagaag gccttgtcag ctttgtctgt gcctcgcaa tcagaggcaa 1800
 gggagagggt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850
 agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtggg 1900
 ggctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950
 acatctcaac agtctcaggt tcgatcagt ggtcttttgg cactttgaac 2000
 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050
 tagcctgact ccagaactt taagactttc tccccactgc cttctgctgc 2100
 agccaagca gggagtgtcc cctcccaga agcatatccc agatgagtgg 2150

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu
 245 250 255
 Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr
 260 265 270
 Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala
 275 280 285
 Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr
 290 295 300
 Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr
 305 310 315
 Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala
 320 325 330
 Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu
 335 340 345
 Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala
 350 355 360
 Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val
 365 370 375
 Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser
 380 385 390
 Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr
 395 400 405
 Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro
 410 415 420
 Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly
 425 430 435
 His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro
 440 445 450
 Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile
 455 460 465
 Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr
 470 475 480
 Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp
 485 490 495
 Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His
 500 505 510
 Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys
 515 520 525
 Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser

530

535

540

Ser Pro Glu Asp

<210> 119
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 119
 cgggacagga gacccagaaa ggg 23

<210> 120
 <211> 24
 <212> DNA
 <213> Artificial

B1
 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 120
 ggccaagtga tccaaggcat cttc 24

<210> 121
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 121
 ctgcgggacc tgactagatt ctacgacaag gtacttttctt tgcattgggg 49

<210> 122
 <211> 1778
 <212> DNA
 <213> Homo sapiens

<400> 122
 gagataggga gtctgggttt aagttcctgc tccatctcag gagcccctgc 50
 tcccacccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100
 gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
 ggagagcccc ggagcccccg taacccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250
 gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300
 ccctggctct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
 aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcctcctcct 400
 gggcgctcgc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500
 ctcatcatgg agctcattgg tggcgtgggt gccttgacct tccggaacca 550
 gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
 aagtgtctgt gcggggagga ctaccgagat tggagcaaga atcagtacca 700
 cgactgcagt gcccttgac ccctggcctg tggggtgccc tacacctgct 750
 gcacaggaa cagacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800
 atcgacaagg agcgtttcag tgtgcaggat gtcacttacg tgcggggctg 850
 caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900
 gcactcctct gggcatcctg ctccccagc tcctgggggt gctgctgacg 950
 ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000
 tgatgggctc ctggggcccg gtgccaagcc cagcgtggag gcggcaggca 1050
 cgggatgctg cttgtgtac cccaattagg gccagcctg ccatggcagc 1100
 tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150
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 gctgtgtgtg cctgtgtgta ggtcccacgg cctctgcctc cccagggagc 1250
 agagcctggg cctcccctaa gaggctttcc ccgaggcagc tctggaatct 1300
 gtgcccacct ggggcctggg gaacaaggcc ctcccttctc caggcctggg 1350
 ctacagggga gggagagcct gaggctctgc tcagggccca ttcatctct 1400
 ggcagtgcct tggcgttgt attcaaggca gttttgtagc acctgtaatt 1450
 ggggagaggg agtgtgccc tcggggcagg agggaagggc atctggggaa 1500
 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccagggttggc 1550
 ctcttctcag cctcccagg gccttgagcc ctcttgcaag ggcggctgct 1600
 tccttgagcc tagtttttt ttacgtgatt ttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700
 gtcttattct tgcccttccc ccaaccagtt tgttaatcaa acaataaaaa 1750
 catgttttgt tttgttttta aaaaaaaa 1778

<210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 123

Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe
 1 5 10 15
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
 20 25 30
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
 170 175 180
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
 185 190 195
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
 200 205 210
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
 215 220 225
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

	230		235		240
Ile Leu Leu Pro Gln Phe Leu Gly Val Leu Leu Thr Leu Leu Tyr					
	245		250		255
Ile Thr Arg Val Glu Asp Ile Ile Met Glu His Ser Val Thr Asp					
	260		265		270
Gly Leu Leu Gly Pro Gly Ala Lys Pro Ser Val Glu Ala Ala Gly					
	275		280		285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn					
	290				

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtggt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcatttatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50
gctgccctct gacacctggg aagatggccg gcccgtggac cttcaccctt 100
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtcctgaagc acatcatctg gctgaaggct atcacagcta 350
acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccttgacat ggtggctgga ttcaacacgc ccctggtcaa 450
gaccatcgtg gagttccaca tgacgactga ggcccaagcc accatccgca 500
tggacaccag tgcaagtggc cccaccgccc tggtcctcag tgactgtgcc 550
accagccatg ggagcctgag catccaactg ctgtataagc tctccttcc 600
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtg ccatccctgc 650
ccaatctagt gaaaaaccag ctgtgtcccc tgatcgaggc ttccttcaat 700
ggcatgtatg cagacctcct gcagctggtg aagggtgccc tttccctcag 750
cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800
ccattcagct ctacctgggg gccaaagtgt tggactcaca gggaaagggtg 850
accaagtgtt tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
caacatcccc ttcagcctca tcgtgagtca ggacgtggtg aaagctgcag 950
tggctgctgt gctctctcca gaagaattca tggtcctggt ggactctgtg 1000
cttctgaga gtgccatcg gctgaagtca agcatcgggc tgatcaatga 1050
aaaggctgca gataagctgg gatctacca gatcgtgaag atcctaactc 1100
aggacactcc cgagtttttt atagaccaag gccatgcaa ggtggcccaa 1150
ctgatcgtgc tggaagtgtt tccctccagt gaagccctcc gccctttgtt 1200
caccctgggc atcgaagcca gctcgggaag tcagttttac accaaagggtg 1250
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400
gatctggggt cccagtgtca ttggtgaagg ccttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttggtg cttactccag cctccttggtg 1500
 gaaaccacgc tctcctgtct cccagtgaag acttggatgg cagccatcag 1550
 ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
 cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128
 <211> 484
 <212> PRT
 <213> Homo sapiens

<400> 128

Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala
 1 5 10 15
 Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
 20 25 30
 Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
 35 40 45
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
 50 55 60
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
 65 70 75
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
 80 85 90
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
 95 100 105
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
 110 115 120
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
 125 130 135
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
 140 145 150
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
 155 160 165
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
 170 175 180
 Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
 185 190 195
 Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
 200 205 210
 Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
 215 220 225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
 230 235 240
 Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
 245 250 255
 Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
 260 265 270
 Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
 275 280 285
 Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
 290 295 300
 Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
 305 310 315
 Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
 320 325 330
 Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
 335 340 345
 Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
 350 355 360
 Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
 365 370 375
 Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
 380 385 390
 Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
 395 400 405
 Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
 410 415 420
 Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
 425 430 435
 Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
 440 445 450
 Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
 455 460 465
 Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
 470 475 480

Pro Val Ser Gln

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129

gagcgaacat ggcagcgcgt tggcggtttt ggtgtgtctc tgtgaccatg 50
gtgggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgcccagaag 100
aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150
ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250
ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300
agatcctggc aaactcctgg cgataactca gtgcattcac caacaggata 350
ttttttgcca tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400
aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaagggaaac 450
ccaaacgggg tgatacatat gagttacagg tgcgggggtt ttcagctgag 500
cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550
tagaccccca aattatgctg gtccccttat gttgggattg cttttggctg 600
ttattgggtg acttgtgtat cttcgaagaa gtaatatgga atttctcttt 650
aataaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700
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atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800
tttgtagctg aaacacacat tgttcttctg tttaatgggtg gagttacctt 850
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ctgagggtatt tgaaaataat tatcctctta accttctctt ccagtggaac 1250
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 cagttagaaa aggactccct ggccaggcgc agtgacttac gcctgtaatc 1950
 tcagcacttt gggaggccaa ggcaggcaga tcacgaggtc aggagttcga 2000
 gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050
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 tgaggcacga gaatcacttg aactcaggag atggagggtt cagtgagccg 2150
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 aaaaaaaaaaaa aaa 2213

<210> 130
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 130
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 Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln
 20 25 30
 Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
 35 40 45
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 50 55 60
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
 65 70 75
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
 80 85 90
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
 95 100 105

Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp
 110 115 120
 Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser
 125 130 135
 Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg
 140 145 150
 Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln
 155 160 165
 Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val
 170 175 180
 Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu
 185 190 195
 Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met
 200 205 210
 Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys
 215 220 225
 Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
 230 235 240
 Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn
 245 250 255
 Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His
 260 265 270
 Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu
 275 280 285
 Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys
 290 295 300
 Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser
 305 310 315
 Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr
 320 325 330
 Ser Phe Leu Met Ser
 335

<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

<400> 131
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tcagaaccgc tacccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150
 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
 cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
 aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
 caatttgttg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
 ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
 atggatggat gtcattggaga ggcatggcta ccgaacacag aaatttggga 500
 aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
 tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggg 600
 taatcttatt cgtaacagga ctaaagtcag agtgatggaa agggattggc 650
 agaatacaga caaagcagta aactggttaa gaaaggaagc aattaattac 700
 actgaaccat ttgttattta cttgggatta aatttaccac acccttacc 750
 ttcaccatct tctggagaaa attttggatc ttcaacattt cacacatctc 800
 tttattggct tgaaaaagtg tctcatgatg ccatcaaaat cccaaagtgg 850
 tcacctttgt cagaaatgca cctgttagat tattactctt cttatacaaa 900
 aaactgcact ggaagattta caaaaaaga aattaagaat attagagcat 950
 tttattatgc tatgtgtgct gagacagatg ccattgcttg tgaaattatt 1000
 ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050
 ctcagaccat ggagagctgg ccatggaaca tcgacagttt tataaaatga 1100
 gcatgtacga ggctagtga catgttccgc ttttgatgat gggaccagga 1150
 attaaagccg gcctacaagt atcaaagtgt gtttctcttg tggatattta 1200
 ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagt 1250
 gatactcttt gttgccgtta tcatcagaaa catttaagaa tgaacataaa 1300
 gtcaaaaacc tgcattccacc ctggattctg agtgaattcc atggatgtaa 1350
 tgtgaatgcc tccacctaca tgcttcgaac taaccactgg aatatatag 1400
 cctattcgga tggatcatca atattgcctc aactctttga tctttcctcg 1450
 gatccagatg aattaacaaa tgttgctgta aaatttccag aaattactta 1500
 ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600
 ataggacaga attattcaaa cgttatagca aatcttaggt ggacaccaaga 1650
 ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700
 aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagtg 1750
 ttctagagat acatataaat atattacaag atcataatta tgtattttta 1800
 atgaaacagt ttttaataatt accaagtttt ggccgggcac agtggctcac 1850
 acctgtaatc ccaggacttt gggaggctga ggaaagcaga tcacaaggtc 1900
 aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950
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 ctcagaggct gaggcaggag gatcgcttga acccgggagg cagcagttgc 2050
 agtgagctga gattgcgcca ctgtactcca gcctggcaac agagtgagac 2100
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 tattttgtaa gaatgtagtg tattttaaga taaaatgcca atgattataa 2200
 aatcacatat tttcaaaaat ggttattatt taggcctttg tacaatttct 2250
 aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300
 atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
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 aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132

Met	Leu	Leu	Leu	Trp	Val	Ser	Val	Val	Ala	Ala	Leu	Ala	Leu	Ala
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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys
				20					25				30	
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg
				35					40				45	
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile
				50					55				60	
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr
				65					70				75	

Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly
 80 85 90
 Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu
 95 100 105
 Asp Pro Asn Tyr Thr Thr Trp Met Asp Val Met Glu Arg His Gly
 110 115 120
 Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His
 125 130 135
 His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala
 140 145 150
 Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg
 155 160 165
 Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr
 170 175 180
 Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr
 185 190 195
 Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr
 200 205 210
 Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His
 215 220 225
 Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys
 230 235 240
 Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr
 245 250 255
 Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys
 260 265 270
 Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu
 275 280 285
 Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu
 290 295 300
 Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly
 305 310 315
 Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr
 320 325 330
 Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile
 335 340 345
 Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile
 350 355 360
 Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn

365 370 375
 Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys
 380 385 390
 Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser
 395 400 405
 Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg
 410 415 420
 Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile
 425 430 435
 Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr
 440 445 450
 Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln
 455 460 465
 Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val
 470 475 480
 His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile
 485 490 495
 Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln
 500 505 510
 Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln
 515 520 525
 Trp Leu Lys Thr His Met Asn Pro Arg Ala Val
 530 535

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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 tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100
 gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150
 ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
 catcaccag tgtgacatct atagcaccct tctgggcctg cccgctgaca 350
 tccaggctgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atcccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatc 550
 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600
 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650
 ctggaatcat cctctgcttt tctgtctcat cccagagaaa tcgctccaac 700
 tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag 750
 gcctgggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800
 cagggtatgt gtgaagaacc agggggccaga gctgggggggt ggctgggtct 850
 gtgaaaaaca gtggacagca ccccgagggc cacagggtgag ggacactacc 900
 actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950
 ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcaggttga 1000
 attgccaagg atgctogcca tgccagcctt tctgttttcc tcaccttgct 1050
 gctcccctgc cctaagtccc caacctcaa cttgaaaccc cattccctta 1100
 agccaggact cagaggatcc ctttgccctc tggtttacct gggactccat 1150
 ccccaaacc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200
 ccctctctct ggctgagggt ggctcttagc tcattgctgg ggatgggaag 1250
 gagaagcagt ggcttttgtg ggcatgctc taacctactt ctcaagcttc 1300
 cctccaaaga aactgattgg ccttggaacc tccatccac tcttgttatg 1350
 actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc 1400
 tacggtatcc agggaaacaga aagcaggatg caggatggga ggacaggaag 1450
 gcagcctggg acatttaaaa aaata 1475

<210> 134
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 134
 Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 1 5 10 15
 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
 20 25 30
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
 35 40 45
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

50 55 60
 Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala
 65 70 75
 Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile
 80 85 90
 Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr
 95 100 105
 Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala
 110 115 120
 Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro
 125 130 135
 Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro
 140 145 150
 Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr
 155 160 165
 Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile
 170 175 180
 Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr
 185 190 195
 Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg
 200 205 210
 Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser
 215 220 225
 Leu Thr Gly Tyr Val
 230

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
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 cttegctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaaggg 100
 aagtcacgc tcccgtggc tcagaacccat ggctgtgcca gccggcaccc 150
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
 cgccatcgtg tccctgagcg agaccgcga atgtgggtccc ccctgcacct 250
 tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcaciaaac 300
 gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136

Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
 1 5 10 15
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137

ctccactgca accacccaga gccatggctc cccgaggctg catcgtagct 50
 gtctttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100
 agtggtcccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300
 agaactgcga ctacgcccgg acctcggatg acaggctttg tcgcagtgtc 350
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550
 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
 ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
 tatgtacttt ataatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens.

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys	1	5	10	15
Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met	20	25	30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	35	40	45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	50	55	60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	65	70	75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	80	85	90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	95	100	105	
Cys	Arg	Ser	Val	Ser	110													

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200
 tctcttcctg gctgcgtccc taggtccggg ggcagccttc aaggtcgcca 250
 cgccgtattc cctgtatgtc tgtcccgagg ggcagaacgt caccctcacc 300
 tgcaggctct tgggccctgt ggacaaaggg cacgatgtga ccttctacaa 350
 gacgtggtac cgcagctcga ggggcgaggt gcagacctgc tcagagcgcc 400
 ggcccatccg caacctcacg ttccaggacc ttcacctgca ccatggaggc 450
 caccaggctg ccaacaccag ccacgacctg gctcagcgcc acgggctgga 500
 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
 ccctgctgga tagcggcctc tactgctgcc tgggtggtgga gatcaggcac 600
 caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650
 aggcaaagat gcaccatcca actgtgtggt gtacctatcc tcctcccagg 700
 atagtgaana catcacggct gcagccctgg ctacgggtgc ctgcatcgta 750
 ggaatcctct gcctccccct catcctgctc ctggtctaca agcaaaggca 800
 ggcagcctcc aaccgccgtg cccaggagct ggtgcggatg gacagcaaca 850
 ttcaagggat tgaanaaccc ggctttgaag cctcaccacc tgcccagggg 900
 atacccgagg ccaaagtcag gcacccccctg tcctatgtgg cccagcggca 950
 gccttctgag tctgggcggc atctgctttc ggagcccagc acccccctgt 1000
 ctctccagg ccccgagagc gtcttcttcc catccctgga cctgtccct 1050
 gactctcaa actttgaggt catctagccc agctggggga cagtgggctg 1100
 ttgtggctgg gtctggggca ggtgcatttg agccagggtt ggctctgtga 1150
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 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250
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 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgctc 1400
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tgggccaccc tcccaggcac cagacacagg gcacggtgga gagacttctc 1500
 ccccggtggcc gccttggtc ccccgttttg cccgaggctg ctcttctgtc 1550
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 ctggccatcg ccaccttccc cagctgcctc ctaccagcag tttctctgaa 1650
 gatctgtcaa cagggttaagt caatctgggg cttccactgc ctgcattcca 1700
 gtccccagag cttggtggtc ccgaaacggg aagtacatat tggggcatgg 1750
 tggcctccgt gagcaaattg tgtcttgggc aatctgaggc caggacagat 1800
 gttgccccac ccactggaga tgggtgctgag ggaggtgggt ggggccttct 1850
 ggggaaggtga gtggagaggg gcacctgccc cccgccctcc ccatccccta 1900
 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly	1	5	10	15
Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	20	25	30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	35	40	45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	50	55	60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	65	70	75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	80	85	90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	95	100	105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	110	115	120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	125	130	135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu				

140 145 150
 Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu
 155 160 165
 Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val
 170 175 180
 Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala
 185 190 195
 Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu
 200 205 210
 Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg
 215 220 225
 Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile
 230 235 240
 Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro
 245 250 255
 Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln
 260 265 270
 Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro
 275 280 285
 Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp
 290 295 300
 Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile
 305 310

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 tctctccctc ctttccccgc gttctctttc cacctttctc ttcttccac 100
 cttagacctc ctttctgcc ctcttttctt gccacacgct gcttcttggc 150
 ccttctccga ccccgctcta gcagcagacc tcctggggtc tgtgggttga 200
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250
 ccgctccccg accagcggcc tgacctggg gaaaggatgg ttcccagggt 300
 gagggctctc tctccttgc tgggactcgc gctgctctgg ttccccctgg 350
 actcccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400
 agatactccc ccggcgagag ctggcacccc tacttggagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
ggccccacca aagtcctgcc agcacaacgg gaccatgtac caacacggag 650
agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccagtgt 700
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
ccccgaacca ggctgccag caccctccc actgccagac tctgctgcc 800
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900
B1 tgggagaaag agaggcccgg gcaccccagc cccactggc ctcagcgccc 950
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100
tcggcccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150
tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200
agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
ctcgtccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350
cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400
taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
ccacacagcc agaatcttcc acttgactca gatcaagaaa gtcaggaagc 1500
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142

<211> 451

<212> PRT

<213> Homo sapiens

<400> 142

Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala
 1 5 10 15
 Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp
 20 25 30
 Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser
 35 40 45
 Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg
 50 55 60
 Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His
 65 70 75
 Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln
 80 85 90
 Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg
 95 100 105
 Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His
 110 115 120
 Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro
 125 130 135
 Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys
 140 145 150
 Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro
 155 160 165
 Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu
 170 175 180
 Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg
 185 190 195
 His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly
 200 205 210
 Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe
 215 220 225
 Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val
 230 235 240
 Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly
 245 250 255
 Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg
 260 265 270
 Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly
 275 280 285
 Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys

	290		295		300
Arg His Pro Glu	Lys Val Ala Gly Lys	Cys Cys Lys Ile Cys	Pro		
	305		310		315
Glu Asp Lys Ala	Asp Pro Gly His Ser	Glu Ile Ser Ser Thr	Arg		
	320		325		330
Cys Pro Lys Ala	Pro Gly Arg Val Leu	Val His Thr Ser Val	Ser		
	335		340		345
Pro Ser Pro Asp	Asn Leu Arg Arg Phe	Ala Leu Glu His Glu	Ala		
	350		355		360
Ser Asp Leu Val	Glu Ile Tyr Leu Trp	Lys Leu Val Lys Asp	Glu		
	365		370		375
Glu Thr Glu Ala	Gln Arg Gly Glu Val	Pro Gly Pro Arg Pro	His		
	380		385		390
Ser Gln Asn Leu	Pro Leu Asp Ser Asp	Gln Glu Ser Gln Glu	Ala		
	395		400		405
Arg Leu Pro Glu	Arg Gly Thr Ala Leu	Pro Thr Ala Arg Trp	Pro		
	410		415		420
Pro Arg Arg Ser	Leu Glu Arg Leu Pro	Ser Pro Asp Pro Gly	Ala		
	425		430		435
Glu Gly His Gly	Gln Ser Arg Gln Ser	Asp Gln Asp Ile Thr	Lys		
	440		445		450

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
 ctatgcctgctg ccaaggggta gtgagaccgc gcggcaacag cttgcggctg 50
 cgaggagctc ccgtgggagc tccgctggct gtgcaggcgg ccatggattc 100
 cttgcggaaa atgctgatct cagtcgcaat gctgggagca ggggctggcg 150
 tgggctacgc gctcctcggt atcgtgaccc cgggagagcg gcggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctcc gtgggcgccg 400
 gaccttggtt tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggctcct 500
 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 ttttaaggctcc gcaaggcggg ccaggggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
 1 5 10 15
 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
 caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcgggc 50
 ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100
 caggctgcc a tggggcccag caccctctc ctcatottgt tccttttgtc 150
 atggtcggga ccctccaag gacagcagca ccaccttgtg gactacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

B1

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500
tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550
ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600
gcaaacagag aagatctacg tgttagatgg gacacagaat gacacagcct 650
ttgtcttccc aaggctgctg gacttcaccc ttgccatggc tgcccggaaa 700
gcttcccagag tccgggtgcc cttcccctgg gtaggcacag ggcagctggt 750
atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800
gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850
aaccgaacag tgggtggacag ctcagtattc ccagcagagg ggctgatccc 900
cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
aaggtctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000
ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050
accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100
tctatgtcgt ctataacacc cgtcctgcca gtcgggcccg catccagtgc 1150
tcctttgatg ccagcggcac cctgaccctt gaacgggcag cactccctta 1200
ttttccccgc agatatggtg cccatgccag cctccgctat aacccccgag 1250
aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
gagatgagga agaaagagga ggaggttga ggagctagcc ttgttttttg 1350
catctttctc actcccatac atttatatta tatcccact aaatttcttg 1400
ttcctcattc ttcaaagtgt ggccagttgt ggctcaaacc ctctatatatt 1450
ttagccaatg gcaatcaaat tctttcagct cctttgtttc atacggaact 1500
ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550
ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600
cccagacca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650
agcagtgttc ttcccctcag agtgacttgg ggaggagaaa ataggaggag 1700
acgtccagct ctgtcctctc ttcctcactc ctcccttcag tgtcctgagg 1750
aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800
gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146
<211> 406
<212> PRT
<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp
1 5 10 15
Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met
20 25 30
Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln
35 40 45
Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
50 55 60
Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala
65 70 75
Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu
80 85 90
Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro
95 100 105
Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys
110 115 120
Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys
125 130 135
Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg
140 145 150
Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln
155 160 165
Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala
170 175 180
Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala
185 190 195
Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr
200 205 210
Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro
215 220 225
Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
230 235 240
Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser
245 250 255

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala
 260 265 270
 Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala
 275 280 285
 Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys
 290 295 300
 Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro
 305 310 315
 Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr
 320 325 330
 Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile
 335 340 345
 Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala
 350 355 360
 Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu
 365 370 375
 Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly
 380 385 390
 Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu
 395 400 405
 Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
 gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgccct 50
 ccgctcacgc agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
 gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300
 gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
 attctattgc ggagggggcg atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
 gaaggccatc tgggagctac aggtgtcagc actggggtca gttcctctca 600
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650
 tcgggctggg tccccggcc cacagcgaag tggaaaggct cacaaggaca 700
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggccgtgttg 750
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800
 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagagat 850
 aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900
 tgggaatact ctgctgtggc ctattttttg gcattgttgg actgaagatt 950
 ttctttctca aattccagtg gaaaatccag gcggaactgg actggagaag 1000
 aaagcacgga caggcagaat tgagagacgc ccggaaacac gcagtggagg 1050
 tgactctgga tccagagacg gctcaccgga agctctgcgt ttctgatctg 1100
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200
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 gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
 cattaaatcc ccgttttata agcgtcttcc ccaggacccc acctacaaaa 1400
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450
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 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaaactcc 1550
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 aaggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650
 caaccacgcc ctctctcccc aggggtgaaa tgtaggatga atcacatccc 1700
 acattcttct ttagggatat taaggtctct ctcccagatc caaagtcccg 1750
 cagcagccgg ccaagggtggc ttccagatga agggggactg gcctgtccac 1800
 atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga 1850
 cattacattt agtttgcctt cactccatct ggctaagtga tcttgaaata 1900
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
acagagtgtgta tcctaattggt ttgttcatta tattacactt tcagtaaaaa 2050
aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly
1 5 10 15
Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala
20 25 30
Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys
35 40 45
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe
50 55 60
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe
65 70 75
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp
80 85 90
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr
95 100 105
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser
110 115 120
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly
125 130 135
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile
140 145 150
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala
155 160 165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg
170 175 180
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu
185 190 195
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His
200 205 210
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp
215 220 225
Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

230 235 240
 Gly Ile Leu Cys Cys Gly Leu Phe Phe Gly Ile Val Gly Leu Lys
 245 250 255
 Ile Phe Phe Ser Lys Phe Gln Trp Lys Ile Gln Ala Glu Leu Asp
 260 265 270
 Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys
 275 280 285
 His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys
 290 295 300
 Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro
 305 310 315
 Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val
 320 325 330
 Val Ala Ser Gln Ser Phe Gln Ala Gly Lys His Tyr Trp Glu Val
 335 340 345
 Asp Gly Gly His Asn Lys Arg Trp Arg Val Gly Val Cys Arg Asp
 350 355 360
 Asp Val Asp Arg Arg Lys Glu Tyr Val Thr Leu Ser Pro Asp His
 365 370 375
 Gly Tyr Trp Val Leu Arg Leu Asn Gly Glu His Leu Tyr Phe Thr
 380 385 390
 Leu Asn Pro Arg Phe Ile Ser Val Phe Pro Arg Thr Pro Pro Thr
 395 400 405
 Lys Ile Gly Val Phe Leu Asp Tyr Glu Cys Gly Thr Ile Ser Phe
 410 415 420
 Phe Asn Ile Asn Asp Gln Ser Leu Ile Tyr Thr Leu Thr Cys Arg
 425 430 435
 Phe Glu Gly Leu Leu Arg Pro Tyr Ile Glu Tyr Pro Ser Tyr Asn
 440 445 450
 Glu Gln Asn Gly Thr Pro Ile Val Ile Cys Pro Val Thr Gln Glu
 455 460 465
 Ser Glu Lys Glu Ala Ser Trp Gln Arg Ala Ser Ala Ile Pro Glu
 470 475 480
 Thr Ser Asn Ser Glu Ser Ser Ser Gln Ala Thr Thr Pro Phe Leu
 485 490 495
 Pro Arg Gly Glu Met
 500

<210> 149

<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgctgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcgggc gcggttgccg aggcttcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctggggc 150
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200
gcctcgggcg ggaatgtcac cgggtggcggc ggggccgcgg ggcaggtgga 250
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300
gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

caccctctt tggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
 cgctcggccc ctgcggacc acccctccgg cggcggaacg cacttcgacc 500
 acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550
 tggcccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600
 ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650
 ctccccaccc cacctgccac cgaggccccc tcttcgcctc ctccagagta 700
 tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750
 agaccacagg gcagtgtgag tgcggccag gttatcaggg gcttactgt 800
 gaaacctgca aagagggtt ttacctaaat tacacttctg ggctctgtca 850
 gccatgtgac tgtagtcac atggagctct cagcataccg tgcaacaggt 900
 aagcaacaga gggtggaact gaagtttatt ttatttttagc aagggaataa 950
 aaaaggctgc tactctcaag gaccatactg gtttaaaaaa aggaggatga 1000
 gggcataga tttaaaaaat attttatata cttttattct cttactttat 1050
 atgttatatt taatgtcagg atttaaaaaac atctaattta ctgatttagt 1100
 tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150
 atttcatggg aaaaaattat tgaagaataa atctgctttc tggaagggt 1200
 ttcaggcatg aaacctgcta ggagggttag aaatgttctt atgtttatta 1250
 atataccatt ggagtttgag gaaatttggt gtttggttta ttttctctc 1300
 taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350
 ggtaccctaa tttatttaac tagtggttag tagactggtt ttactctatt 1400
 taccagtaca ttttgagac caaaagtaga ttaagcagga attatcttta 1450
 aactattatg ttatttgag gtaatttaat ctagtggaat aatgtactgt 1500
 tatctaagca ttgccttgt actgcactga aagtaattat tctttgacct 1550
 tatgtgaggc acttggttt ttgtggaccc caagtcaaaa aactgaagag 1600
 acagtattaa ataataaaaa aaataatgac aggttatact cagtgtacc 1650
 tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700
 agtaatttcc tttcactgag cttgtttctt ctcaagggtt ttgtgaagat 1750
 taaatgagtt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800
 ctggtttgtt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcttt atacttttagc 1900
 actaaatatt ttaaagtctt tataaatgat attatactgt tatggaatat 1950
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000
 ctcacgcctg taatcctagc actttgggag gccaaaggcgg gtggatcact 2050
 tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgctct 2100
 ctactaaaaa tacaacaaaa ttagctgggc gtggtggcac acacctgtag 2150
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200
 tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250
 agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153
 <211> 258
 <212> PRT
 <213> Homo sapiens

<400> 153

Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys
 1 5 10 15
 Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn
 20 25 30
 Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro
 35 40 45
 Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala
 50 55 60
 Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala
 65 70 75
 Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro
 80 85 90
 Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr
 95 100 105
 Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala
 110 115 120
 Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro
 125 130 135
 Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val
 140 145 150
 Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro
 155 160 165
 Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro

170	175	180
Ala Thr Glu Ala Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys Asn	
185	190	195
Cys Ser Val Val Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln Thr	
200	205	210
Thr Gly Gln Cys Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His Cys	
215	220	225
Glu Thr Cys Lys Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly Leu	
230	235	240
Cys Gln Pro Cys Asp Cys Ser Pro His	Gly Ala Leu Ser Ile Pro	
245	250	255
Cys Asn Arg		

B1
 <210> 154
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 154
 aactgctctg tggttggaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-38
 <223> Synthetic construct.

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
 tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
 ttctggcttt ggtctcggtg cccagggccc aggccgtgtg gttgggaaga 100
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cgggtggcctc 150
 ccgggaaaag ggctttgcca tggagaagga catgaagaac gtcgtggggg 200
 tggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
 cacgggctgg gaggggtgtg ccagagtgtc atggacctga taaagcgaaa 300
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
 tgctggccac caacttcaga gactatgcca tcatcttcac tcagctggag 400
 ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttctgtgc acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600
 gggtcctgtg acctcggcca gtgtccaccc acctcgtca gcggctcccg 650
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
			95						100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
			110						115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
			125						130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
			140						145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
			155						160					

<210> 159
 <211> 1665
 <212> DNA
 <213> Homo sapiens

B1

<400> 159
 aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50
 gctgctgctg ccctgctct gggggagga gagggcgaa ggacagaca 100
 gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150
 gtccatgtgc cctgctcctt ctctacccc tcgcatggct ggatttaccc 200
 tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250
 aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
 cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
 gtatggagaa aggaagtata aaatggaatt ataaacatca ccggtctct 450
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
 cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
 gtgagcaggg gacaccccct atgatctcct ggatagggac ctccgtgtcc 600
 ccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650
 gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
 ccagcgtgac caggaacaag accgtccatc tcaacgtgtc ctacccgcct 750
 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
 tggctctgtg agttgatgca gttgacagca atccccctgc caggctgagc 900
 ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950

ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
 gcagagctca gaacctctc ggctctcagc aggtctacct gaacgtctcc 1050
 ctgcagagca aagccacatc aggagtgact caggggggtgg tcgggggagc 1100
 tggagccaca gccctggtct tctgtcctt ctgcgtcatc ttcgtttag 1150
 tgaggctctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
 acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcaggggcc 1250
 cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag 1300
 cttctgcccg ctctcagtg ggggaaggag agctccagta tgcattccctc 1350
 agcttcagga tggatgaaggc ttgggactcg cggggacagg aggcactga 1400
 caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600
 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650
 acagacaaat tccta 1665

<210> 160
 <211> 463
 <212> PRT
 <213> Homo sapiens

<400> 160
 Met Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala
 1 5 10 15
 Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr
 20 25 30
 Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr
 35 40 45
 Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr
 50 55 60
 Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala
 65 70 75
 Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg
 80 85 90
 Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser
 95 100 105
 Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

110 115 120
 Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu
 125 130 135
 Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile
 140 145 150
 Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser
 155 160 165
 Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp
 170 175 180
 Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser
 185 190 195
 Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser
 200 205 210
 Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
 215 220 225
 Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr
 230 235 240
 Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly
 245 250 255
 Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu
 260 265 270
 Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu
 275 280 285
 Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser
 290 295 300
 Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala
 305 310 315
 Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln
 320 325 330
 Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val
 335 340 345
 Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe
 350 355 360
 Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys
 365 370 375
 Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu
 380 385 390
 Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr
 395 400 405

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200
 aaggtgacag ccctgggcggt tgggaagttg gaagccacgt tcaccttcac 250
 gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa ttttaagaaat tgggtgcagcg caagggactc 500
 tcggaggagg acattttcac gcccctgcag acgggaagct gcgttcccga 550
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttcctt 650
 gctcccaccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20 25 30
 Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg
 35 40 45
 Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly
 50 55 60
 Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile
 65 70 75
 Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr
 80 85 90
 Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro
 95 100 105
 Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly
 110 115 120
 Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr
 125 130 135
 Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys
 140 145 150
 Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser
 155 160 165
 Cys Val Pro Glu His
 170

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtgtt cgggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
cagggaacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttca ccctggagga ggaggatatc acagggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50
cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150
gtagggggag agaccaggat catcaagggg ttcgagtga agcctcactc 200
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtggg 250
cgacgtcat cgtcccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgtaca tagttcacct ggggcagcac aacctccaga aggaggagg 350
ctgtgagcag acccgagacg cactgagtc cttccccac cccgggttca 400
acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500
ctcacgtgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600
atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccaggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
attatctcct ggggccagga tccgtgtgcg atcaccgaa agcctggtgt 800
ctacacgaaa gtctgcaaat atgtggactg gatccaggag acgatgaaga 850
acaattagac tggacccacc caccacagcc catcaccctc catttccact 900
tgggtgttgg ttctgttca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000
taataatcaa cctgggggtc gaaatcagtg agacctggat tcaaattctg 1050
ccttgaaata ttgtgactct gggaatgaca acacctgggt tgttctctgt 1100
tgtatcccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
1 5 10 15

Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
 20 25 30
 His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
 35 40 45
 Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
 50 55 60
 Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
 65 70 75
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
 80 85 90
 Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
 95 100 105
 Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val
 110 115 120
 Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys
 125 130 135
 Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr
 140 145 150
 Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn
 155 160 165
 Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly
 170 175 180
 Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly
 185 190 195
 Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn
 200 205 210
 Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
 215 220 225
 Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
 230 235 240
 Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
 245 250

<210> 171
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 171
ggctgcggga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctgggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgccggggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggctttc ggggtg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctggtc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctaata aatgccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtcatt 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccgatgc tacattgatt ttgagattg aactttatgc 450
 tgtgacaaaa ggaccacgga gcattgagac atttaaaca atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
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 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650
 ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
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 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800
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 aaaaaaa 907

<210> 180
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 180

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Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	35	40	45	
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	50	55	60	
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	65	70	75	
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	80	85	90	
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	95	100	105	
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	110	115	120	
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	125	130	135	
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	140	145	150	

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181
 <211> 22
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

 <400> 181
 gtgtttctgct ggagccgatg cc 22

 <210> 182
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 182
 gacatggaca atgacagg 18

 <210> 183
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 183
 cctttcagga tgtaggag 18

 <210> 184
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
gcatactgat atgacttgct acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
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cccaaatgct tcctgtgtca ataactactca ctgcacctgc aacctatggat 150
 atacttcttg atctgggcag aaactattca cattccccctt ggagacatgt. 200
 aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250
 aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 ggtgcatgcc tgcaatccca gttactcggg aggtgagggc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
 ttcttgtttc atttcgcgac tgccctctca gtgtttcctg ggatcccctc 550
 ccaaataaag tacttatatt ctc 573

<210> 189
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 189
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 1 5 10 15
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
 20 25 30
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
 35 40 45
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
 50 55 60
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
 65 70

<210> 190
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 190
 aggaccatt gcttcttcca ggcc 24

<210> 191
 <211> 24
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgccccca aatgcttct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
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gactttggaa gtgaccacc atggggctca gcatcttttt gtcctgtgt 150
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
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gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcactgca gcggcagcag gtactgggtg cgcttggggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
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tgcctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
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atgcctgcca gggtgattct gggggccccc tgggtgtgtgg gggagtcctt 750
caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

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 ccctagctcc actcttggtg gcctgggaac ttcttggaac ttttaactcct 1000
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 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 194

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 1 5 10 15
 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
 20 25 30
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
 35 40 45
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
 50 55 60
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
 65 70 75
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
 80 85 90
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
 95 100 105
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
 110 115 120
 Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
 125 130 135
 Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
 140 145 150
 Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
 155 160 165
 Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
 170 175 180
 Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
 185 190 195
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
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 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcggtc 150
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccac ctggagatga agaagatgat ctgagagggtg acaggagggg 400
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 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500
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 tgacccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 196
 Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe
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 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
 20 25 30
 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
 35 40 45
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
 50 55 60
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
 65 70 75
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
 80 85 90
 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
 95 100 105
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
 110 115 120
 Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
 125 130 135
 Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
 140 145 150

<210> 197
 <211> 4842
 <212> DNA
 <213> Homo sapiens

<400> 197

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ggggtcggcg ccgccgtgcg cgccgcctg gcgctggcct tggcgctggc 150
gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200
gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttcct 250
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tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccttccag 400
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ccttcagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500
tgagtgaaaa ccagatccag gggatcccga ggaaggcgtt ccgcggcatc 550
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<210> 198
<211> 1523
<212> PRT
<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg	1	5	10	15
Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro	20	25	30	
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val	35	40	45	
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro	50	55	60	
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg	65	70	75	
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu	80	85	90	
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe	95	100	105	
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys	110	115	120	
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu	125	130	135	
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg	140	145	150	
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp	155	160	165	

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu
 170 175 180
 Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Ile Ser Arg
 185 190 195
 Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu
 200 205 210
 Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp
 215 220 225
 Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr
 230 235 240
 Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp
 245 250 255
 Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro
 260 265 270
 Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr
 275 280 285
 Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu
 290 295 300
 Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu
 305 310 315
 Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr
 320 325 330
 Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp
 335 340 345
 Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu
 350 355 360
 Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe
 365 370 375
 Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys
 380 385 390
 Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu
 395 400 405
 Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys
 410 415 420
 Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala
 425 430 435
 Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp
 440 445 450
 Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser

Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr
 755 760 765
 Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile
 770 775 780
 Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe
 785 790 795
 Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg
 800 805 810
 Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu
 815 820 825
 Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu
 830 835 840
 Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly
 845 850 855
 Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu
 860 865 870
 Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser
 875 880 885
 Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr
 890 895 900
 His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala
 905 910 915
 Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr
 920 925 930
 Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr
 935 940 945
 Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile
 950 955 960
 Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser
 965 970 975
 His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly
 980 985 990
 Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys
 995 1000 1005
 Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys
 1010 1015 1020
 Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile
 1025 1030 1035
 Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys

1040 1045 1050
 Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly
 1055 1060 1065
 Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala
 1070 1075 1080
 His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly
 1085 1090 1095
 Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu
 1100 1105 1110
 His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln
 1115 1120 1125
 Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu
 1130 1135 1140
 Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu
 1145 1150 1155
 Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu
 1160 1165 1170
 Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln
 1175 1180 1185
 Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp
 1190 1195 1200
 Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu
 1205 1210 1215
 Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val
 1220 1225 1230
 Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr
 1235 1240 1245
 Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys
 1250 1255 1260
 Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser
 1265 1270 1275
 Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala
 1280 1285 1290
 Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys
 1295 1300 1305
 Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala
 1310 1315 1320
 Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys
 1325 1330 1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
 1340 1345 1350
 Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
 1355 1360 1365
 Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
 1370 1375 1380
 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
 1385 1390 1395
 Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
 1400 1405 1410
 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
 1415 1420 1425
 Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
 1430 1435 1440
 Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
 1445 1450 1455
 Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
 1460 1465 1470
 Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
 1475 1480 1485
 Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
 1490 1495 1500
 Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
 1505 1510 1515
 Glu Cys Gly Cys Leu Ala Cys Ser
 1520

<210> 199
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 199
 atggagattc ctgccaaactt gccg 24

<210> 200
 <211> 24
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttgcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
ggatgcagga cgctccoctg agctgcctgt caccgactag gtggagcagt 50
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
gaatctgcct ttccagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350
gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaag gctgtgaggt ttcttaaact ggaactggac 600
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650
cctgtgtcat cttgtcccg ttcctcccaa tttccttct caaacttga 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccattttaa 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203

Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
 1 5 10 15
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaaactgg caaaaatatt ctcgaggggt ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
caggccattt gcatcccaact gtccttgtgt tcggagccag gccacaccgt 50
cctcagcagt gtcatgtgtt aaaaacgcca agctgaatat atcatgcccc 100
tattaaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatttt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
 gaggaatata ccacagggcat ggcagactgc atcttagtca acagccagtt 350
 cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
 ctgatgtcct ctatccatct ctaaattgtca ccagctttga ctcagttggt 450
 cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500
 ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcaactggaag 550
 ccctagtaca gctgcgtgga agattgacat cccaagattg ggagaggggt 600
 catctgatcg tggcaggtgg ttatgacgag agagtcctgg agaattgtgga 650
 acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700
 atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctctc 750
 cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800
 tgtccctctg gaagccatgt acatgcagtg ccagtcatt gctgttaatt 850
 cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900
 gagcctgacc cgggtgacct ctcagaagca atagaaaagt tcatccgtga 950
 accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000
 aaaaattttc ccctgaagca ttacagaac agctctaccg atatgttacc 1050
 aaactgctgg tataatcaga ttgtttttaa gatctccatt aatgtcattt 1100
 ttatggattg tagaccaggt ttgaaacca aaaaagaaac ctagaatcta 1150
 atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200
 ctttcctata taccacacct ccctgtccac ttttcagaaa aacctgtct 1250
 tttatgctat aatcattcca aattttgcca gtgttaagtt acaaattgtg 1300
 tgtcattcca tggtcagcag agtattttta ttatatatttc tcgggattat 1350
 tgctcttctg tctataaaatt ttgaatgata ctgtgcctta attggttttc 1400
 atagtttaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450
 ataagagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500
 tcaactgtcat ctgttaggga atttttgttt gtccctgtctt tgcctggatc 1550
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600
 actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210

<211> 323

<212> PRT
 <213> Homo sapiens

<400> 210

Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly
 1 5 10 15
 Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val
 20 25 30
 Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His
 35 40 45
 Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg
 50 55 60
 Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly
 65 70 75
 Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val
 80 85 90
 Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val
 95 100 105
 Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro
 110 115 120
 Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu
 125 130 135
 Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala
 140 145 150
 Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp
 155 160 165
 Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg
 170 175 180
 Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val
 185 190 195
 Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe
 200 205 210
 Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val
 215 220 225
 Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
 230 235 240
 Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly
 245 250 255
 Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu
 260 265 270

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
275 280 285

Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
290 295 300

Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
305 310 315

Arg Tyr Val Thr Lys Leu Leu Val
320

<210> 211
<211> 1554
<212> DNA
<213> Homo sapiens

<400> 211
gactacgccg atccgagacg tggctccctg ggccggcagaa ccatgttgga 50
cttcgcgatac ttccgccgtta ctttcttgct ggccgttggtg ggagccgtgc 100
tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaa 200
tttgcatag ttcctgggtta atttgcatga gagatatggg cctgtggtct 250
ccttctgggtt tggcaggcgc ctcgtgggtta gtttgggcac tgttgatgta 300
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtga 400
accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
gttttgctat gaagtctgtt acacagatgg taatgggttag tacatttgaa 600
gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
tgactcctta gtacaaggga acctaatga ccaacagatc ctagaagaca 850
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
 tggtaacttca ggatcctaatt acttggccat ctccacacaa gtttgatcca 1200
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
 ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212
 <211> 462
 <212> PRT
 <213> Homo sapiens

<400> 212
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
 1 5 10 15
 Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
 20 25 30
 Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
 35 40 45
 Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
 50 55 60
 Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
 65 70 75
 Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
 80 85 90
 Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
 95 100 105
 Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
 110 115 120
 His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
 125 130 135
 Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

140 145 150
 Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser
 155 160 165
 Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val
 170 175 180
 Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln
 185 190 195
 Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu
 200 205 210
 Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu
 215 220 225
 Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys
 230 235 240
 Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser
 245 250 255
 Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser
 260 265 270
 Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys
 275 280 285
 Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys
 290 295 300
 Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val
 305 310 315
 Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu
 320 325 330
 Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln
 335 340 345
 Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg
 350 355 360
 Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro
 365 370 375
 Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp
 380 385 390
 Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly
 395 400 405
 Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr
 410 415 420
 Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val
 425 430 435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
 455 460

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
 ctagatttgt cggcttgccg ggagacttca ggagtcgctg tctctgaact 50
 tccagcctca gagaccgccg cccttgcccc cgagggccat gggccgggtc 100
 tcagggttg tgccctctcg ctctctgacg ctcttgccgc atctggtggt 150
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250
 gccgcgtct ctgtcaccct gggcctcttt gcagtgagc tggccggttt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400
 tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450
 agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
 tccccctcgg aaactgcttc tgctggagga tatgtgttg aataattacg 650
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
 tgttttgtag taacattaag acttatatac agtttttaggg gacaattaaa 750
 aaaaaaaaaa 759

<210> 214
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 214
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
 1 5 10 15
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
 20 25 30
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
 35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
 50 55 60
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
 65 70 75
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
 80 85 90
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
 95 100 105
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
 110 115 120
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
 125 130 135
 Lys Lys Lys Pro Phe
 140

<210> 215
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 215
 tcccggaccc tgccgccctg ccactatgtc ccgccgtct atgctgcttg 50
 cctgggctct cccagcctc cttegactcg gagcggctca ggagacagaa 100
 gacccggcct gctgcagccc catagtgtcc cggaacgagt ggaaggccct 150
 ggcacagag tgcgcccagc acctgagcct gcccttaagc tatgtggtgg 200
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
 gtggttgaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
 tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
 ccaggccatc cgggcagccc aggtctact ggcctgcggt gtggctcagg 500
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<210> 216
 <211> 196
 <212> PRT

<213> Homo sapiens

<400> 216

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu
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Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
20 25 30
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
35 40 45
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
50 55 60
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
65 70 75
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
80 85 90
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
95 100 105
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
110 115 120
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
125 130 135
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
140 145 150
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
155 160 165
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
170 175 180
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
185 190 195

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatctggt catctgtggc caggatgatg gtctctcccg ctcagaggac 150
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aataaagctt gccccggggc a 1871

<210> 218
<211> 252
<212> PRT
<213> Homo sapiens

<400> 218

Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser
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Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser
20 25 30
Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
35 40 45
Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
50 55 60
Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
65 70 75
Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
80 85 90
Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
95 100 105
Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
110 115 120
Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
125 130 135
His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
140 145 150
Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
155 160 165
Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
170 175 180
Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
185 190 195
Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
 215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
 230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
 245 250

<210> 219
 <211> 2065
 <212> DNA
 <213> Homo sapiens

<400> 219
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 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150
 agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200
 gcgccgcgcg cgcgctcgct cctgcagcgc tgcgcaccta gccgctagca 250
 tcttcccagag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300
 agcgccagcc ggctgcggct gccacacgg ctcaccatgg gctccgggcg 350
 ccgggcgctg tccgcggtgc cggccgtgct gctggtcctc acgctgccgg 400
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 ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600
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 tttcacattg gagtctgtct ttgtagcacc aagaaaagg atttacagtt 700
 tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750
 ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800
 tgttactcgt gaagctgcc cgaatggtgt cctgctctac ctagataaag 850
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 cagtattcca cgttttctgg ctttctggtg ttccccctat aggattcaat 950
 ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000
 gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050
 ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100

tcacagatta tttgtgtgtg tctgtttcag tatatttgga ttgggactct 1150
 aagcagataa tacctatgct taaatgtaac agtcaaaagc tgtctgcaag 1200
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 ttcaaataatc ccataatctaa atttagtgca atatcttgtc ttttgtatag 2000
 gtcatatgaa ttcataaaat tatttatgtc tgttatagaa taaagattaa 2050
 tatatgttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met	Gly	Ser	Gly	Arg	Arg	Ala	Leu	Ser	Ala	Val	Pro	Ala	Val	Leu
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Leu	Val	Leu	Thr	Leu	Pro	Gly	Leu	Pro	Val	Trp	Ala	Gln	Asn	Asp
				20				25					30	

Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
				35				40					45	

Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
				50				55					60	

Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala
 65 70 75
 Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr
 80 85 90
 Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe
 95 100 105
 Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr
 110 115 120
 Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile
 125 130 135
 Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe
 140 145 150
 Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val
 155 160 165
 Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
 170 175 180
 Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly
 185 190 195
 Phe Leu Val Phe Pro Leu
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<210> 221
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 221
 acggctcacc atgggctccg 20

<210> 222
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 222
 aggaagagga gcccttggag tccg 24

<210> 223
 <211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
cgtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

B1
<400> 224
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tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
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ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly
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Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu
20 25 30
Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser
35 40 45
Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
50 55 60
Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
65 70 75
Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr
80 85 90
Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
95 100 105
Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser
110 115 120
Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn
125 130 135
Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly
140 145 150
Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val
155 160 165
Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly
170 175 180
Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr
185 190 195
His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly
200 205 210
Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr
215 220 225
Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu
230 235 240
Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg
245 250 255
Ser Arg

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226

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agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200
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<210> 227
 <211> 832
 <212> PRT
 <213> Homo sapiens

<400> 227
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 1 5 10 15
 Val Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln
 20 25 30

Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser
 35 40 45
 Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn
 50 55 60
 Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln
 65 70 75
 Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
 80 85 90
 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg
 95 100 105
 Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
 110 115 120
 Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser
 125 130 135
 Thr Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg
 140 145 150
 Met Asp Asp Phe Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn
 155 160 165
 Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu
 170 175 180
 Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe
 185 190 195
 Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr
 200 205 210
 Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met
 215 220 225
 Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
 230 235 240
 Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala
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 Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro
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 Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser
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 Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys
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 Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala
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 Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala

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 Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly
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 Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser
 365 370 375
 Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe
 380 385 390
 Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val
 395 400 405
 Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys
 410 415 420
 Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala
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 Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe
 440 445 450
 Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val
 455 460 465
 Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn
 470 475 480
 Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly
 485 490 495
 Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile
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 515 520 525
 Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu
 530 535 540
 Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
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 Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys
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 Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met
 575 580 585
 Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro
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 Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile
 605 610 615

Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn
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 Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr
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 Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu
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 Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp
 665 670 675
 Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val
 680 685 690
 Leu Leu Val Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr
 695 700 705
 Gly Leu Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala
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 Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile
 725 730 735
 Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu
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 Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu Phe Phe
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 Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
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 His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser
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<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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 <212> PRT
 <213> Homo sapiens

<400> 229
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 35 40 45
 Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp
 50 55 60
 Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser
 65 70 75
 Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala
 80 85 90
 Glu Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val
 95 100 105
 Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn
 110 115 120
 Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu
 125 130 135
 Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala
 140 145 150
 Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe
 155 160 165
 His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe
 170 175 180
 Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly
 185 190 195
 Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu
 200 205 210
 Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala
 215 220 225
 Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser
 230 235 240
 Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro
 245 250 255
 His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr
 260 265 270
 His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu
 275 280 285
 Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala
 290 295 300
 Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Glu Asp
 305 310 315

Tyr Ala Ala Pro Leu Glu Leu His Val Leu Val Met Asp Glu Asn
 320 325 330
 Asp Asn Val Pro Ile Cys Pro Pro Arg Asp Pro Thr Val Ser Ile
 335 340 345
 Pro Glu Leu Ser Pro Pro Gly Thr Glu Val Thr Arg Leu Ser Ala
 350 355 360
 Glu Asp Ala Asp Ala Pro Gly Ser Pro Asn Ser His Val Val Tyr
 365 370 375
 Gln Leu Leu Ser Pro Glu Pro Glu Asp Gly Val Glu Gly Arg Ala
 380 385 390
 Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu
 395 400 405
 Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met
 410 415 420
 Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val
 425 430 435
 Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile
 440 445 450
 Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro
 455 460 465
 Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu
 470 475 480
 Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr
 485 490 495
 Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val
 500 505 510
 Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser
 515 520 525
 His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly
 530 535 540
 Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val
 545 550 555
 Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu
 560 565 570
 Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr
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 Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu
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<210> 232
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<220>
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<400> 232
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<210> 233
<211> 2786
<212> DNA
<213> Homo sapiens

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 <211> 421
 <212> PRT
 <213> Homo sapiens

<400> 234

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Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn	35	40	45	
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe	50	55	60	
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala	65	70	75	
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr	80	85	90	
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met	95	100	105	
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr	110	115	120	
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn	125	130	135	
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly	140	145	150	
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr	155	160	165	

Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile
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 His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala
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 Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser
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 Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro
 215 220 225
 Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys
 230 235 240
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 245 250 255
 Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp
 260 265 270
 Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu
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 Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn
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 Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met
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 Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr
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 Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile
 365 370 375
 Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly
 380 385 390
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Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 235

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 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236

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 20 25 30
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

B1

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctggtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

B1
<400> 239
tgactcgggg tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactctttgc tggtggcctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50

agctgccac gctgagtc aagattcttc ccaggaacac aaacgtagga 100
 gacccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150
 ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta 200
 ggacccaggg atcttgcttt ccagccacaa agagacagat gaagatgcag 250
 aaaggaaatg ttctccttat gtttggctta ctattgcatt tagaagctgc 300
 aacaaattcc aatgagacta gcacctctgc caaactgga tccagtgtga 350
 tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400
 agtgggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450
 ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500
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 gccaccaact ctgagtccag cagacctcc agtggggcca gcacagccac 1050
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 ctgagtccag cagacctcc agtggggcca gcacagccac caactctgag 1150
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 cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag 1250
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 gcaactgccac caactctgag tccagcaca cctccagtgg ggtcagcaca 1450
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 gcattcttca ggaaggaaga gacctgggca cccaagacct ggtttccttt 2100
 cattcatccc aggagacccc tcccagcttt gtttgagatc ctgaaaatct 2150
 tgaagaaggt attcctcacc tttcttgctt ttaccagaca ctggaaagag 2200
 aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250
 acacgacaaa gagaagctgt gcttgccccg ggggtgggtat ctagctctga 2300
 gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350
 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243
 <211> 596
 <212> PRT
 <213> Homo sapiens

<400> 243
 Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu
 1 5 10 15
 Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser
 20 25 30
 Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
 35 40 45
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
 50 55 60
 Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
 65 70 75

Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala
 80 85 90
 Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala
 95 100 105
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 110 115 120
 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val
 125 130 135
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala
 140 145 150
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 155 160 165
 Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala
 170 175 180
 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 185 190 195
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 200 205 210
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 215 220 225
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 230 235 240
 Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala
 245 250 255
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 260 265 270
 Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
 275 280 285
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 290 295 300
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 305 310 315
 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala
 320 325 330
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
 335 340 345
 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala
 350 355 360
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala

365 370 375
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
 380 385 390
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala
 395 400 405
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 410 415 420
 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala
 425 430 435
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
 440 445 450
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala
 455 460 465
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala
 470 475 480
 Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala
 485 490 495
 Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile
 500 505 510
 Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe
 515 520 525
 Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn
 530 535 540
 Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly
 545 550 555
 Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro
 560 565 570
 Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile
 575 580 585
 Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro
 590 595

<210> 244
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic sequence.

<400> 245
gtcagagttg gtggctgtgc tagc 24

<210> 246
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 246
ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247
<211> 957
<212> DNA
<213> Homo sapiens

<400> 247
gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50
ttcccgaacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100
tccctccttc tgctactggg ggccctgtct ggatgggagg ccagcgatga 150
ccccattgag aaggtcattg aagggatcaa ccgaggggctg agcaatgcag 200
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250
gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300
ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350
tggaacaagg tgcccatgag atcaaccatg gtattggaca agcaggaaag 400
gaagcagaga agcttggcca tgggggtcaac aacgctgctg gacaggccgg 450
gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500
ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 550
caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650
 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700
 tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750
 agtcaacacg cctttcatca accttcccg cctgtggagg agcgtcgcca 800
 acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850
 gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900
 tttctgaaat ccctgaaggg ggttgactg ggatttgtga ataaacttga 950
 tacacca 957

<210> 248
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 248

Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu
 1 5 10 15
 Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu
 20 25 30
 Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg
 35 40 45
 Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
 50 55 60
 Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
 65 70 75
 Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
 80 85 90
 Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
 95 100 105
 Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
 110 115 120
 Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
 125 130 135
 Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
 140 145 150
 Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
 155 160 165
 Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala
 170 175 180

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
230 235 240

Ser Val Ala Asn Ile Met Pro
245

B1 <210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgacccatt gagaaggtca ttgaaggat caaccgaggg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252

B1
ctccgggtcc ccaggggctg cgccggggccg gcctggcaag ggggacgagt 50
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tgaccctgac tactccagg tccggaggcg ggggcccccg gggcgactcg 150
ggggcgacc gcggggcgga gctgccgcc gtgagtccg ccgagccacc 200
tgagcccgag ccgcgggaca ccgtcgctcc tgctctccga atgctgcgca 250
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<210> 253
 <211> 837
 <212> PRT
 <213> Homo sapiens

<400> 253
 Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro
 1 5 10 15
 Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu
 20 25 30
 Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser
 35 40 45
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu
 50 55 60
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
 65 70 75
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80 85 90

Phe Ala Leu Ser Ser Asn Leu Ser Phe Leu Pro Gly Gly Glu Tyr
95 100 105

Gln Glu Leu Leu Trp Gly Ala Asp Ala Glu Lys Lys Gln Gln Cys
110 115 120

Ser Phe Lys Gly Lys Asp Pro Gln Arg Asp Cys Gln Asn Tyr Ile
125 130 135

Lys Ile Leu Leu Pro Leu Ser Gly Ser His Leu Phe Thr Cys Gly
140 145 150

Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr Ile Asn Met Glu Asn
155 160 165

Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val Leu Leu Glu Asp
170 175 180

Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys Ser Thr Ala
185 190 195

Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser Ser Phe
200 205 210

Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg Pro
215 220 225

Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe
230 235 240

Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly
245 250 255

Asp Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu
260 265 270

Phe Glu Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile
275 280 285

Cys Lys Gly Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp
290 295 300

Thr Ser Phe Leu Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp
305 310 315

Gly Phe Pro Phe Asn Val Leu Gln Asp Val Phe Thr Leu Ser Pro
320 325 330

Ser Pro Gln Asp Trp Arg Asp Thr Leu Phe Tyr Gly Val Phe Thr
335 340 345

Ser Gln Trp His Arg Gly Thr Thr Glu Gly Ser Ala Val Cys Val
350 355 360

Phe Thr Met Lys Asp Val Gln Arg Val Phe Ser Gly Leu Tyr Lys
365 370 375

Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro
 380 385 390
 Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg
 395 400 405
 Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu
 410 415 420
 Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser
 425 430 435
 Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala
 440 445 450
 Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe
 455 460 465
 Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
 470 475 480
 Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly
 485 490 495
 Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu
 500 505 510
 Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn
 515 520 525
 Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp
 530 535 540
 Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu
 545 550 555
 Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu
 560 565 570
 Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser
 575 580 585
 Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln
 590 595 600
 Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser
 605 610 615
 Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn
 620 625 630
 Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu
 635 640 645
 Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu
 650 655 660
 Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val

665 670 675
 Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro
 680 685 690
 Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly Lys
 695 700 705
 Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val
 710 715 720
 Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe
 725 730 735
 Leu Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln
 740 745 750
 Gly Glu Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu
 755 760 765
 Pro Pro Glu Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr
 770 775 780
 Pro Leu Asp His Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro
 785 790 795
 Gly Ala Arg Val Phe Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile
 800 805 810
 Gln Asp Ser Phe Val Glu Val Ser Pro Val Cys Pro Arg Pro Arg
 815 820 825
 Val Arg Leu Gly Ser Glu Ile Arg Asp Ser Val Val
 830 835

<210> 254
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 254
 agcccgtagca gaatctgctc ctgg 24

<210> 255
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 255
tgaagccagg gcagcgtcct ctgg 24

<210> 256
<211> 18
<212> DNA
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<220>
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<222> 1-18
<223> Synthetic construct.

<400> 256
gtacaggctg cagttggc 18

<210> 257
<211> 41
<212> DNA
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<220>
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<222> 1-41
<223> Synthetic construct.

<400> 257
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<210> 258
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 258
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 3635
<223> unknown base

<400> 259
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 cgcccagacc gccgctagcg cgcgccgggc atggtcccct cttaaaggcg 250
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B1

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aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

Met Ala Ala Arg Gly Arg Arg Ala Trp Leu Ser Val Leu Leu Gly
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Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg
20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

Lys Cys Leu Arg Glu Met Tyr Thr Thr His Glu Asp Val Glu Val
 245 250 255
 Gly Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser
 260 265 270
 Tyr Glu Met Arg Gln Leu Phe Tyr Glu Asn Tyr Glu Gln Asn Lys
 275 280 285
 Lys Gly Tyr Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala
 290 295 300
 Ile Thr Leu His Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu
 305 310 315
 His Ser Tyr Met Leu Ser Arg Lys Ile Ser Glu Leu Arg His Arg
 320 325 330
 Thr Ile Gln Leu His Arg Glu Ile Val Leu Met Ser Lys Tyr Ser
 335 340 345
 Asn Thr Glu Ile His Lys Glu Asp Leu Gln Leu Gly Ile Pro Pro
 350 355 360
 Ser Phe Met Arg Phe Gln Pro Arg Gln Arg Glu Glu Ile Leu Glu
 365 370 375
 Trp Glu Phe Leu Thr Gly Lys Tyr Leu Tyr Ser Ala Val Asp Gly
 380 385 390
 Gln Pro Pro Arg Arg Gly Met Asp Ser Ala Gln Arg Glu Ala Leu
 395 400 405
 Asp Asp Ile Val Met Gln Val Met Glu Met Ile Asn Ala Asn Ala
 410 415 420
 Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile Gln Tyr Gly
 425 430 435
 Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile Leu Asp
 440 445 450
 Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr Val
 455 460 465
 Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile
 470 475 480
 Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys
 485 490 495
 Arg Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser
 500 505 510
 Leu Lys Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu
 515 520 525
 His Lys Glu Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu

530 535 540
 Ser Gly Arg Phe Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu
 545 550 555
 Lys Thr Cys Leu Ile Pro Asn Gln Asn Val Lys Leu Val Val Leu
 560 565 570
 Leu Phe Asn Ser Asp Ser Asn Pro Asp Lys Ala Lys Gln Val Glu
 575 580 585
 Leu Met Arg Asp Tyr Arg Ile Lys Tyr Pro Lys Ala Asp Met Gln
 590 595 600
 Ile Leu Pro Val Ser Gly Glu Phe Ser Arg Ala Leu Ala Leu Glu
 605 610 615
 Val Gly Ser Ser Gln Phe Asn Asn Glu Ser Leu Leu Phe Phe Cys
 620 625 630
 Asp Val Asp Leu Val Phe Thr Thr Glu Phe Leu Gln Arg Cys Arg
 635 640 645
 Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe Pro Ile Ile Phe
 650 655 660
 Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys Val Pro Ser
 665 670 675
 Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp Arg Asn
 680 685 690
 Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val Arg
 695 700 705
 Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp
 710 715 720
 Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe
 725 730 735
 Arg Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe
 740 745 750
 Cys Asp Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly
 755 760 765
 Ser Lys Ala Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met
 770 775 780
 Trp Leu Glu Lys Asn Asp Pro Ser Tyr Ser Lys Ser Ser Asn Asn
 785 790 795
 Asn Gly Ser Val Arg Thr Ala
 800

<210> 261
 <211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450
 gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccgccattc 500
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30
Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45
Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser

50 55 60
 Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys
 65 70 75
 Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu
 80 85 90
 Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly
 95 100 105
 Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro
 110 115 120
 Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala
 125 130 135
 Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu
 140 145 150
 Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val
 155 160 165
 Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro
 170 175 180
 Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu
 185 190 195
 Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys
 200 205 210
 Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp
 215 220 225
 Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala
 230 235 240
 Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu
 245 250 255
 Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala
 260 265 270
 Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro
 275 280 285
 Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile
 290 295 300
 Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp
 305 310 315
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 320 325 330
 Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala
 335 340 345

Leu Leu Lys Val Tyr
350

<210> 266
<211> 2403
<212> DNA
<213> Homo sapiens

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 caaattaaac taaacaatat atttaaagat gatataaac tactcagtgt 2300
 ggtttgtccc acaaatgcag agttggttta atatttaa atcaaccagt 2350
 gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400
 aaa 2403

<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

Met	Ala	Phe	Val	Leu	Ile	Leu	Val	Leu	Ser	Phe	Tyr	Glu	Leu	Val
1				5				10					15	

Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

20 25 30
 Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu
 35 40 45
 Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe
 50 55 60
 His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser
 65 70 75
 Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp
 80 85 90
 Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr
 95 100 105
 Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile
 110 115 120
 Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly
 125 130 135
 Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile
 140 145 150
 Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala
 155 160 165
 Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg
 170 175 180
 Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile
 185 190 195
 Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu
 200 205 210
 Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu
 215 220 225
 Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu
 230 235 240
 Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile
 245 250 255
 Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp
 260 265 270
 Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys
 275 280 285
 His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys
 290 295 300
 Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro
 305 310 315

Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val
 320 325 330
 Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val
 335 340 345
 Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp
 350 355 360
 Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn
 365 370 375
 Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr
 380 385 390
 Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr
 395 400 405
 Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe
 410 415 420
 Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys
 425 430 435
 Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr
 440 445 450
 Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp
 455 460 465

Gly

<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
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 gtcattctca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
 tgtcattttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
 attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350
 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
 agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
 tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

ctcaactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
 ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
 caggatcggt ggtgggacag aagtagaaga gggatgaatgg ccctggcagg 650
 ctgacctgca gtgggatggg agtcatcgct gtggagcaac ctttaattaat 700
 gccacatggc ttgtgagtgc tgctcactgt ttacaacat ataagaaccc 750
 tgccagatgg actgcttcct ttggagtaac aataaacct tcgaaaatga 800
 aacggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850
 catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900
 aatgcagta catagagttt gtctccctga tgcacctat gagtttcaac 950
 caggatgatg gatgtttgtg acaggatttg gagcactgaa aatgatggg 1000
 tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050
 aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100
 tatgtgctgg ctccctagaa ggaaaaacag atgcatgcca gggatgactct 1150
 ggaggaccac tggtagttc agatgctaga gatattctgg accttgctgg 1200
 aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctgggtgtt 1250
 atactagagt tacggccttg cgggactgga ttacttcaaa aactggtatc 1300
 taagagacaa aagcctcatg gaacagataa catttttttt tgttttttgg 1350
 gtgtggaggc cattttttaga gatacagaat tggagaagac ttgcaaaaca 1400
 gctagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc 1450
 ttcccagctc tgttccgcac gtaagcatcc tgcttctgcc agatcaactc 1500
 tgtcatctgt gagcaatagt tgaaacttta tgtacataga gaaatagata 1550
 atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt 1600
 cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650
 agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaataatcc 1700
 attttcaagg tgcagaacaa ggagtgaag aaaatataag aagaaaaaaa 1750
 tcccctacat ttatttggca cagaaaagta ttaggtgttt ttcttagtgg 1800
 aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850
 aataccaatc acttcatcat ttaggaagta tgggaactaa gtttaaggag 1900
 tccagaaaga agccaagata taccottatt ttcatttcca aacaactact 1950

atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050
 ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100
 cca 2103

<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269
 Met Met Tyr Arg Pro Asp Val Val Arg-Ala Arg Lys Arg Val Cys
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 Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile
 20 25 30
 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
 110 115 120
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
 155 160 165
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 215 220 225

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro
 230 235 240
 Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys
 245 250 255
 Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys
 260 265 270
 His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser
 275 280 285
 Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp
 290 295 300
 Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly
 305 310 315
 Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg
 320 325 330
 Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro
 335 340 345
 Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly
 350 355 360
 Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly
 365 370 375
 Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly
 380 385 390
 Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly
 395 400 405
 Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys
 410 415 420

Thr Gly Ile

<210> 270
 <211> 1170
 <212> DNA
 <213> Homo sapiens

<400> 270
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 cagacgtcag ctggtggatt cccgctgcat caaggcctac ccactgtctc 150
 catgctgggc tctccctgcc ttctgtggct cctggcogtg accttcttgg 200
 ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

gatgagactg agacggcgtg gccgcctttg ccggtgtgcc cctgagacta 300
 cgaccactgc cgacacctgc aggtgccctg caaggagcta cagagggtcg 350
 ggcggggcgc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400
 gacccgccgc gcatgggaga agtgcgcatg gcggccgaag agggccgcgc 450
 agtgggtccac tgggtgtgcc cttctctccc ggtcctccac tactggctgc 500
 tgctttggga cggcagcgag gctgcgaga aggggcccc gctgaacgct 550
 acgggtccgca gagccgaact gaaggggctg aagccagggg gcatttatgt 600
 cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650
 ctggaggaga gggcctcgag ggggccgaca tccctgcctt cgggccttgc 700
 agccgccttg cggtgccgcc caacccccgc actctgggtcc acgcggccgt 750
 cggggtgggc acggccctgg ccctgctaag ctgtgccgcc ctggtgtggc 800
 acttctgcct gcgcgatcgc tggggctgcc cgcgccgagc cgccgcccga 850
 gccgcagggg cgctctgaaa ggggcctggg ggcattctcg gcacagacag 900
 cccacactgg ggcgtcagc ctggcccccg ggaaagagga aaaccgctg 950
 cctccaggga gggctggacg gcgagctggg agccagcccc aggtccagg 1000
 gccacggcgg agtcatggtt ctcaggactg agcgcttggt taggtccggt 1050
 acttggcgct ttgtttcctg gctgaggtct gggaaggaat agaaaggggc 1100
 cccaatttt ttttaagcg gccagataat aaataatgta acctttgcgg 1150
 ttaaaaaaaaa aaaaaaaaaa 1170

<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

Met	Leu	Gly	Ser	Pro	Cys	Leu	Leu	Trp	Leu	Leu	Ala	Val	Thr	Phe
1				5					10					15

Leu	Val	Pro	Arg	Ala	Gln	Pro	Leu	Ala	Pro	Gln	Asp	Phe	Glu	Glu
				20					25					30

Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
				35					40					45

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys
				50					55					60

Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly
				65					70					75

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu
 80 85 90
 Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys
 95 100 105
 Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
 110 115 120
 Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val
 125 130 135
 Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
 140 145 150
 Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
 155 160 165
 Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
 170 175 180
 Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
 185 190 195
 Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
 200 205 210
 Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly
 215 220 225
 Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
 230 235

<210> 272
 <211> 2397
 <212> DNA
 <213> Homo sapiens

<400> 272
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 cccaggcggg cgtggggcac cgggcccagc gccgacgac gctgccgttt 150
 tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
 gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgctgtctct 250
 acgccctcaa tctgctcttt tggtaaatgt ccatcagtg gttggcagtt 300
 tctgcttggg tgagggacta cctaaataat gttctcactt taactgcaga 350
 aacgagggta gaggaagcag tcattttgac ttactttcct gtgggttcac 400
 cggatcatgat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450
 tattgtggaa cggtgaaaag aaatctgttg cttcttgcac ggtactttgg 500

aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttggacat 550
atgaacagga acttatgggt ccagtacaat ggtcagatat ggtcactttg 600
aaagccagga tgacaaatta tggattacct agatatcggg ggcttactca 650
tgcttggaaat ttttttcaga gagagttaa gtgctgtgga gtagtatatt 700
tcaactgactg gttggaaatg acagagatgg actggcccc agattcctgc 750
tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct 800
cagtgcctt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850
gaggaaccaa acaactgcag gtgctgaggt ttctgggaat ctccattggg 900
gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct 950
gtattatgat agaagggagc ctgggacaga ccaaatgatg tccttgaaga 1000
atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca 1050
agcctgtcaa gaatctttga acacacatcc atggcaaaca gctttaatac 1100
acactttgag atggaggagt tataaaaaga aatgtcacag aagaaaacca 1150
caaacttggt ttattggact tgtgaatttt tgagtacata ctatgtgttt 1200
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250
tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc 1300
accacctgga caataattga tgcccttaa atgctgaaga cagatgtcat 1350
accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg 1400
aggcagcatg gtttgattag catttccgca tccatgcaaa cgagtcacat 1450
atggtgggac tggagccata gtaaagggtg atttacttct accaactagt 1500
atataaagta ctaattaaat gctaacatag gaagttagaa aatactaata 1550
acttttatta ctacgcgatc tattcttctg atgctaaata aattatata 1600
cagaaaactt tcaatattgg tgactaccta aatgtgattt ttgctgggta 1650
ctaaaatatt cttaccactt aaaagagcaa gctaacacat tgtcttaagc 1700
tgatcagga tttttgtat ataagtctgt gttaaactctg tataattcag 1750
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actattctgt cctgggctta tattacacat ataactgtta tttaaatact 1900
taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc 1950

agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa 2000
 cttagttgat tcagaaagga cttgtatgct gtttttctcc caaatgaaga 2050
 ctctttttga cactaaacac tttttaaaaa gcttatcttt gccttctcca 2100
 aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagtg 2150
 ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200
 tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta 2250
 cacagattat taaatTTTTT tacaagagta tagtatattt atttgaaatg 2300
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 atggaaagaa aattaaaatg tgtcaataaa tattttctag agagtaa 2397

<210> 273
 <211> 305
 <212> PRT
 <213> Homo sapiens

<400> 273

Met Ala Arg Glu Asp Ser Val Lys Cys Leu Arg Cys Leu Leu Tyr
 1 5 10 15
 Ala Leu Asn Leu Leu Phe Trp Leu Met Ser Ile Ser Val Leu Ala
 20 25 30
 Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
 35 40 45
 Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
 50 55 60
 Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
 65 70 75
 Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
 80 85 90
 Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
 95 100 105
 Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
 110 115 120
 Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met
 125 130 135
 Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp
 140 145 150
 Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe
 155 160 165
 Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser

170	175	180
Cys Cys Val Arg Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln 185 190 195		
Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met 200 205 210		
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe 215 220 225		
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu 230 235 240		
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro 245 250 255		
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His 260 265 270		
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg 275 280 285		
Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe 290 295 300		
Glu Met Glu Glu Leu 305		

<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

<400> 274
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 caaggcctgc cctgcactcg ggcctcctcc agccagtgtc gaccaggac 100
 ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgtctgc 150
 cttggggtga caatctcagc tccaggctac agggagaaccg ggaggatcac 200
 agagccagca tgttacagga tcctgacagt gatcaacctc tgaacagcct 250
 cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa 300
 aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc 350
 attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg 400
 cgggcagcct ctccacttca tcccaggaa gcagctgtgt gacggagagc 450
 tggactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc 500
 gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550
 ggtgctggac tcggccacag ggaactggtt ctctgcctgt ttcgacaact 600

tcacagaagc tctcgtgag acagcctgta ggcagatggg ctacagcaga 650
 gctgtggaga ttggcccaga ccaggatctg gatgttgttg aaatcacaga 700
 aaacagccag gagcttcgca tgcggaactc aagtgggccc tgtctctcag 750
 gctccctggg ctccctgcac tgtcttgccct gtgggaagag cctgaagacc 800
 ccccggtggg tgggtgggga ggaggcctct gtggattctt ggccttggca 850
 ggtcagcatc cagtacgaca aacagcacgt ctgtggaggg agcatcctgg 900
 acccccactg ggtcctcacg gcagcccact gcttcaggaa acataccgat 950
 gtgttcaact ggaagggtgcg ggcaggctca gacaaactgg gcagcttccc 1000
 atccctgggt gtggccaaga tcatcatcat tgaattcaac cccatgtacc 1050
 ccaaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcactttc 1100
 tcaggcacag tcaggcccat ctgtctgccc ttctttgatg aggagctcac 1150
 tccagccacc ccactctgga tcattggatg gggctttacg aagcagaatg 1200
 gagggaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac 1250
 agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa 1300
 gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccaggggtg 1350
 acagtgggtg gcccctgatg taccaatctg accagtggca tgtgggtgggc 1400
 atcgttagct ggggctatgg ctgcgggggc ccgagcacc caggagtata 1450
 caccaaggtc tcagcctatc tcaactggat ctacaatgtc tggaaggctg 1500
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 ttgggtacac ccctctgccc acagcctcag catttcttgg agcagcaaag 1650
 ggcctcaatt cctgtaagag accctcgcag ccagaggcg ccagaggaa 1700
 gtcagcagcc ctagctcggc cacacttggg gctcccagca tcccaggag 1750
 agacacagcc cactgaacaa ggtctcaggg gtattgctaa gccaagaagg 1800
 aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850
 tcaactgtgg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900
 tcttcaccca tcccgaagcc tactagagca agaaaccagt tgtaatataa 1950
 aatgcactgc cctactgttg gtatgactac cgttacctac tgttgctatt 2000
 gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg 2050

caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp
1 5 10 15
Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg
20 25 30
Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser
35 40 45
Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
50 55 60
Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
65 70 75
Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
80 85 90
His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
95 100 105
Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110 115 120
Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125 130 135
Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
140 145 150
Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
155 160 165
Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
170 175 180
Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
185 190 195
Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
200 205 210
Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
215 220 225
Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
230 235 240
Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
245 250 255

265

Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys
 260 265 270
 Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp
 275 280 285
 Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr
 290 295 300
 Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro
 305 310 315
 Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn
 320 325 330
 Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val
 335 340 345
 Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu
 350 355 360
 Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val
 365 370 375
 Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser
 380 385 390
 Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys
 395 400 405
 Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr
 410 415 420
 Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu
 425 430

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 276
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 gagcatggcc ctcccagccc tgggcctgga cccttgagc ctctggggcc 150
 ttttcctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200
 ggaggcgggc aggggcccac gccaggggtc agatactatg caggggatga 250
 acgtagggca cttagcttct tccaccagaa gggcctccag gattttgaca 300
 ctctgctcct gactggtgat ggaaatactc tctacgtggg ggctcgagaa 350
 gccattctgg ccttgatat ccaggatcca ggggtcccca ggctaaagaa 400

catgataccg tggccagcca gtgacagaaa aaagagtgaa tgtgccttta 450
agaagaagag caatgagaca cagtgtttca acttcatccg tgccttggtt 500
tcttacaatg tcacccatct ctacacctgc ggcaccttcg ccttcagccc 550
tgcttgtagc ttcatggaac ttcaagattc ctacctgttg cccatctcgg 600
aggacaaggt catggaggga aaaggccaaa gcccctttga ccccgtcac 650
aagcatacgg ctgtcttggt ggatgggatg ctctattctg gtactatgaa 700
caacttctg ggcagtgagc ccatcctgat gcgcacactg ggatcccagc 750
ctgtcctcaa gaccgacaac ttctccgct ggctgcatca tgacgcctcc 800
tttgtggcag ccatcccttc gaccaggtc gtctacttct tcttcgagga 850
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ccctcctctg ataaggccct gaccttcatg aaggaccatt tcctgatgga 1300
tgagcaagtg gtggggacgc ccctgctggt gaaatctggc gtggagtata 1350
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gtcatgtacc tgggaaccac cacagggtcg ctccacaagg ctgtggtaag 1450
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tggcccatg agcaggagcc ttcggcctca gagccgcccg caaatcatta 1800
aagaagtctt ggctgtcccc aactccatcc tggagctccc ctgccccac 1850

B1

ctgtcagcct tggcctctta ttattggagt catggcccag cagcagtcct 1900
 agaagcctct tccactgtct acaatggctc cctcttgctg atagtgcagg 1950
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 catcatcctc gtggcctccc cattgagagc actccgggct cggggcaagg 2250
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<210> 277
 <211> 761
 <212> PRT
 <213> Homo sapiens
 <400> 277

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 Ala Gly Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr
 35 40 45
 Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly
 50 55 60
 Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr
 65 70 75
 Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln
 80 85 90
 Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala
 95 100 105
 Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn
 110 115 120
 Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn
 125 130 135
 Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala
 140 145 150
 Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser
 155 160 165
 Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro
 170 175 180
 Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser
 185 190 195
 Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg
 200 205 210
 Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg
 215 220 225
 Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
 230 235 240
 Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp
 245 250 255
 Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys
 260 265 270
 Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr
 275 280 285
 Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro

290 295 300
 Phe Asn Val Ile Arg His Ala Val Leu Leu Pro Ala Asp Ser Pro
 305 310 315
 Thr Ala Pro His Ile Tyr Ala Val Phe Thr Ser Gln Trp Gln Val
 320 325 330
 Gly Gly Thr Arg Ser Ser Ala Val Cys Ala Phe Ser Leu Leu Asp
 335 340 345
 Ile Glu Arg Val Phe Lys Gly Lys Tyr Lys Glu Leu Asn Lys Glu
 350 355 360
 Thr Ser Arg Trp Thr Thr Tyr Arg Gly Pro Glu Thr Asn Pro Arg
 365 370 375
 Pro Gly Ser Cys Ser Val Gly Pro Ser Ser Asp Lys Ala Leu Thr
 380 385 390
 Phe Met Lys Asp His Phe Leu Met Asp Glu Gln Val Val Gly Thr
 395 400 405
 Pro Leu Leu Val Lys Ser Gly Val Glu Tyr Thr Arg Leu Ala Val
 410 415 420
 Glu Thr Ala Gln Gly Leu Asp Gly His Ser His Leu Val Met Tyr
 425 430 435
 Leu Gly Thr Thr Thr Gly Ser Leu His Lys Ala Val Val Ser Gly
 440 445 450
 Asp Ser Ser Ala His Leu Val Glu Glu Ile Gln Leu Phe Pro Asp
 455 460 465
 Pro Glu Pro Val Arg Asn Leu Gln Leu Ala Pro Thr Gln Gly Ala
 470 475 480
 Val Phe Val Gly Phe Ser Gly Gly Val Trp Arg Val Pro Arg Ala
 485 490 495
 Asn Cys Ser Val Tyr Glu Ser Cys Val Asp Cys Val Leu Ala Arg
 500 505 510
 Asp Pro His Cys Ala Trp Asp Pro Glu Ser Arg Thr Cys Cys Leu
 515 520 525
 Leu Ser Ala Pro Asn Leu Asn Ser Trp Lys Gln Asp Met Glu Arg
 530 535 540
 Gly Asn Pro Glu Trp Ala Cys Ala Ser Gly Pro Met Ser Arg Ser
 545 550 555
 Leu Arg Pro Gln Ser Arg Pro Gln Ile Ile Lys Glu Val Leu Ala
 560 565 570
 Val Pro Asn Ser Ile Leu Glu Leu Pro Cys Pro His Leu Ser Ala
 575 580 585

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
 590 600
 Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
 605 610 615
 Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
 620 625 630
 Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
 635 640 645
 Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
 650 655 660
 Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
 665 670 675
 Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
 680 685 690
 Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
 695 700 705
 Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
 710 715 720
 Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
 725 730 735
 Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp
 740 745 750
 Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
 755 760

<210> 278
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 278
 ctgctggtga aatctggcgt ggag 24

<210> 279
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 279
gtctgttcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

B1
<400> 281
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atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450
ggatatcatg gattccttaa agaataagaa cttcgacatg gtgatagttg 500
aaacttttga ctactgtcct ttcctgattg ctgagaagct tgggaagcca 550
tttgtggcca ttctttccac ttcattcggc tctttggaat ttgggctacc 600
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agtaccacaa gacttggaga acttcattgc caagtttggg gactctggtt 950
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 atgtgaaaat tgtggactgg ctctctcaga gtgacctcct ggctcaccca 1150
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 catccagcat ggtgtgcccc tgggtgggat ccctctcttt ggagaccagc 1250
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 tctctccca acctcactaa 2320

<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

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 Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr
 20 25 30
 Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
 35 40 45
 Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
 50 55 60
 Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
 65 70 75
 Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
 80 85 90
 Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
 95 100 105
 Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
 110 115 120
 Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
 125 130 135
 Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
 140 145 150
 Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile
 155 160 165
 Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro
 170 175 180
 Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met
 185 190 195
 Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe
 200 205 210
 Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile
 215 220 225
 Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu
 230 235 240
 Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe
 245 250 255
 Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly

B1

260										265					270				
Leu	Met	Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Glu	Asn					
				275					280					285					
Phe	Ile	Ala	Lys	Phe	Gly	Asp	Ser	Gly	Phe	Val	Leu	Val	Thr	Leu					
				290					295					300					
Gly	Ser	Met	Val	Asn	Thr	Cys	Gln	Asn	Pro	Glu	Ile	Phe	Lys	Glu					
				305					310					315					
Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys					
				320					325					330					
Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn					
				335					340					345					
Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His					
				350					355					360					
Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile					
				365					370					375					
Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu					
				380					385					390					
Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys					
				395					400					405					
Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu					
				410					415					420					
Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser					
				425					430					435					
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser					
				440					445					450					
Pro	Thr	Gln	Arg	Leu	Val	Gly	Trp	Ile	Asp	His	Val	Leu	Gln	Thr					
				455					460					465					
Gly	Gly	Ala	Thr	His	Leu	Lys	Pro	Tyr	Val	Phe	Gln	Gln	Pro	Trp					
				470					475					480					
His	Glu	Gln	Tyr	Leu	Phe	Asp	Val	Phe	Val	Phe	Leu	Leu	Gly	Leu					
				485					490					495					
Thr	Leu	Gly	Thr	Leu	Trp	Leu	Cys	Gly	Lys	Leu	Leu	Gly	Met	Ala					
				500					505					510					
Val	Trp	Trp	Leu	Arg	Gly	Ala	Arg	Lys	Val	Lys	Glu	Thr							
				515					520										

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 283
tgcctttgct cacctacccc aagg 24

<210> 284
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 284
tcaggctggt ctccaaagag aggg 24

<210> 285
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 285
cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 286
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gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
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gttcagcgag cctagagagg gcagactatc aggggtgccgg cggtgagaat 400
ccagggagag gagcggaac agaagagggg cagaagaccg gggcacttgt 450

gggttgcaga gccctcagc catgttggga gccaaagccac actggctacc 500
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 gagctgtggc atctccagac caggcctttc caccaccca ccccagtta 1300
 ccctcccagc cacctgctgc atctgttctt gcctgcagcc ctaggatcag 1350
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 ctccggttcc cccaccccag cttcctgctc aatgctgac agggacaggt 1450
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 cagcgtaccc tgcaggcttc ttctgtgag gaaagccagc atcacggatc 1550
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 aggctcagcc acaggcagaa ggggtgggaag ggcctggagt ctgtggctgg 1650
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 tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850
 ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900

B1

ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950
 cactctgact gctgcctcct tcctcccagc tctctcactg agttatcttc 2000
 actgtacctg ttccagcata tccccactat ctctctttct cctgatctgt 2050
 gctgtcttat tctcctcctt aggcttccta ttacctggga ttccatgatt 2100
 cattccttca gaccctctcc tgccagtatg ctaaaccctc cctctctctt 2150
 tcttatcccg ctgtccatt ggcccagcct ggatgaatct atcaataaaa 2200
 caactagaga atggtggtca gtgagacact atagaattac taaggagaag 2250
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300
 agaggaaaat aaatatcaaa ctgtatacta aaattaataaa 2340

B1
 <210> 287
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 287

Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser
 1 5 10 15

Pro Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly
 20 25 30

Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys
 35 40 45

Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly
 50 55 60

Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala
 65 70 75

Ala Val Arg Ser His His His Glu Pro Ala Gly Glu Thr Gly Asn
 80 85 90

Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val Asn Glu
 95 100 105

Gly Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val
 110 115 120

Arg Gly Val Tyr Ser Phe Arg Phe His Val Val Lys Val Tyr Asn
 125 130 135

Arg Gln Thr Val Gln Val Ser Leu Met Leu Asn Thr Trp Pro Val
 140 145 150

Ile Ser Ala Phe Ala Asn Asp Pro Asp Val Thr Arg Glu Ala Ala
 155 160 165

Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser

	170		175		180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser					
	185		190		195

Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu	
	200 205

<210> 288
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 288
 aggcagccac cagctctgtg ctac 24

B1

<210> 289
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 289
 cagagaggga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 290
 ctgtgctact gcccttgac cctggggacc gagtgtctct gc 42

<210> 291
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 291
 gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50
 tagccgcca gcctcgacgc cgtcccggga cccctgtgct ctgcgcgaag 100
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttccccgctgg ggcgtgactg ggcgggcttc agccatgaag accctcatag 200
 ccgcctactc cggggctcctg cgcgggcgagc gtcaggccga ggctgaccgg 250
 agccagcgct ctcacggagg acctgcgctg tcgcgcgagg ggtctgggag 300
 atgggggact ggatccagca tcctctccgc cctccaggac ctcttctctg 350
 tcacctggct caataggctc aaggtggaaa agcagctaca ggtcatctca 400
 gtgctccagt gggctcctgtc cttccttgta ctgggagtg gctgcagtgc 450
 catcctcatg tacatattct gcaactgattg ctggctcatc gctgtgctct 500
 acttcacttg gctgggtgtt gactggaaca caccacaaga aggtggcagg 550
 aggtcacagt gggctccgaaa ctgggctgtg tggcgctact ttcgagacta 600
 ctttcccatc cagctgggtga agacacacaa cctgctgacc accaggaact 650
 atatcttttg ataccacccc catggtatca tgggcctggg tgccttctgc 700
 aacttcagca cagaggccac agaagtgagc aagaagttcc caggcatacg 750
 gccttacctg gctacactgg caggcaactt ccgaatgcct gtgttgaggg 800
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 ggggtgcggct gagtctctga gctccatgcc tggcaagaat gcagtcaccc 950
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 ctggttccca tctactcctt tggagagaat gaagtgtaca agcaggtgat 1050
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 acattggttt cgccccatgc atcttccatg gtcgaggcct cttctcctcc 1150
 gacacctggg ggctgggtgcc ctactccaag cccatcacca ctggtgtggg 1200
 agagcccatc accatcccca agctggagca cccaaccag caagacatcg 1250
 acctgtacca caccatgtac atggaggccc tgggtgaagct cttcgacaag 1300
 cacaagacca agttcggcct cccggagact gaggtcctgg aggtgaactg 1350
 agccagcctt cggggccaat tccctggagg aaccagctgc aaatcacttt 1400
 tttgctctgt aaatttggaa gtgtcatggg tgtctgtggg ttatttataa 1450
 gaaattataa caattttgct aaacaaaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550
 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

Met Lys Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu
 1 5 10 15
 Arg Gln Ala Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro
 20 25 30
 Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser
 35 40 45
 Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn
 50 55 60
 Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln
 65 70 75
 Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile
 80 85 90
 Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
 95 100 105
 Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly
 110 115 120
 Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr
 125 130 135
 Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu
 140 145 150
 Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile
 155 160 165
 Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu
 170 175 180
 Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu
 185 190 195
 Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser
 200 205 210
 Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu
 215 220 225
 Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly
 230 235 240
 Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr
 245 250 255
 Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly

260 265 270
 Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr
 275 280 285
 Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln
 290 295 300
 Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His
 305 310 315
 Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr
 320 325 330
 Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro
 335 340 345
 Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr
 350 355 360
 Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr
 365 370 375
 Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn
 380 385

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

B1
<400> 296
gggcggcggg atggggggccg ggggcggcgg gcgccgcact cgctgaggcc 50
ccgacgcagg gccggggccg gcccagggcc gaggagcgcg gcggccagag 100
cggggccgcg gaggcgacgc cggggacgcc cgcgcgacga gcagggtggc 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
ggctctgctg accttgtgcc ttggacggct gtccctcagc aggggccgtg 250
caccgcgtcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300
gttcgtgctg cacctgtggt tcggctttgt ctctgtggtg agtgggtctg 350
tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400
cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450
actggtcatg ctgctggagt ggtggtcctg cacggagtgt aactgttca 500
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550
ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600
gcgcttcgga gtgctgggga gctccaaggt cctcgctaag aaggagctgc 650
tctacgtgcc cctcatcggc tggacgtggt actttctgga gattgtgttc 700
tgcaagcgga agtgggagga ggaccgggac accgtggtcg aagggtgag 750
gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgcgagg 800
ggacgcgctt cacggagacc aagcaccgcg ttagcatgga ggtggcggct 850
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tgtaccagga gaaggacgcg ctccaggaga tatataatca gaagggcag 1150

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 cttcctgtcc tgggccacca ttctcctgtc tcccctcttc agttttgtct 1250
 tgggcgtctt tgccagcgga tcacctctcc tgatcctgac tttcttgggg 1300
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 tgaacctggg aggtggagat tgcagtgagc tgagatggca tcaactgtact 1400
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 aaaaacccca gaaattcttg agttgaactg tgtagttact gacatgaaaa 1500
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 agcttgaaga tggtagcttg agatttttca ggctaataaa aaaagaatga 1600
 aggaaaatta acagcctcag agacccatgg tgcaccgtca cacaaatcaa 1650
 catatgcatg atgagagtcc cagaaggaga ggagagaaaag ggtcagaaaag 1700
 aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750
 gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800
 aatcaaagtg tcaaatagca aagaatcttg aaagcagcaa gagatgagca 1850
 acttatcttg ttcaaaggat ctttgatcag attaacagct catttctcct 1900
 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050
 aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100
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 gtgatcccaa gtagcttggg ttgtaaacat gcaccacat gcctggctaa 2350
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 gacctcaagt gaccacctgc ctacgcctcc caaagtactg ggattacagg 2450
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 cttttttaa tttttattat ttatttattt atttattttg agacagggtc 2600

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 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gcccacta 2950
 ccagggagac tgaagtggga ggatcgcttg ggcattgagaa gtcgaggctg 3000
 cagtgagtcg aggttggtgc actgcattcc agcctggaca acagagtgag 3050
 accctgtctc 3060

<210> 297
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu
1				5					10					15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe
				20					25					30
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu
				35					40					45
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln
				50					55					60
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu
				65					70					75
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala
				80					85					90
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly
				95					100					105
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val
				110					115					120
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr
				125					130					135
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu
				140					145					150
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr
				155					160					165

Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe
 170 175 180
 Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys
 185 190 195
 Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly
 200 205 210
 Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val
 215 220 225
 Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
 230 235 240
 Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val
 245 250 255
 Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala
 260 265 270
 Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln
 275 280 285
 Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys
 290 295 300
 Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala
 305 310 315
 Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe
 320 325 330
 Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val
 335 340 345
 Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Glu Ser Leu
 350 355 360
 Glu Pro Gly Arg Trp Arg Leu Gln
 365

<210> 298
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 298
 cttcctctgt gggtaggacca tgtg 24

<210> 299
 <211> 21
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

gatattcttt atttttaaga atctgaagta ctatgcatca ctccctccaa 50
tgctctgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100
tgcttttagca ctggggcact tcttgcttat ttctttgga ggaaaggggc 150
tcagtttgct ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200
cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250
tagctggggg ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300
ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350
ttctctctgt tcttaggata aaagtattta gagctacaag agccctcatg 400
gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450
tgtcgttctt gtaatgtggg atgccatggg gtctttgcac aagcctttcc 500
tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550
atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600
ctggcctgac agaattctcat cttgtttaat gctctcataa gaccacttgt 650
ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700
gttgatatgg ttgtgtctgt tccccagaat gccagctct gagctgcgtg 750

aggggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggtgtaggg cccagcattg taaattcaca 900
 cgttgactgt gcttgtgaat tatctgggga tgcaggctct gattcagtag 950
 gcccagggtg ggcattctcta acaaactccc acgtgatgct gatgctggtc 1000
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050
 tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgata 1100
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 tctgtactaa aaatacacia attagctggg catggtggca catgcctgta 1200
 gtcccagcta cttgggaggg tgaagcaaga gaatcgcttg aacctgggag 1250
 gcggagggtg cagtgaagcc agatcaggcc actgtattcc aaccagggtg 1300
 acagagttag actctatgtc caaaaaaaaa aaaa 1334

<210> 302
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
1				5					10					15
His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
				20					25					30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35					40					45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50					55					60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
				65					70					75
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
				80					85					90
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
				95					100					105
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
				110					115					120
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
				125					130					135
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
 ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50
 aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatgtgtggtg tggctagtgc tcctactcct acctacatta aaatctgttt 200
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
 ttctaccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350
 ctctcgtggtg agcagtcccc tcaccaactg tctcacgtct ggaggcactg 400
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450
 tgggccttgc cctggccgta gaagggttg acaagcccga agatttcata 500
 ggcgatggct cccactgccc aggcacacgc cttgctgtag tcaatcactg 550
 ccctggggcc agggacggggc gtggacacct gctcagaagc agtgggtgag 600
 acatcacgct gcccgcccat ctaacctttt catgtcctgc acatcacctg 650
 atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga 700
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 acaggacttg cattctcctg gaacatgagg gaacgccgga ggaaagcaaa 800
 gtggcagggg aggaacttgt gccaaattat gggtcagaaa agatggaggt 850
 gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900
 ggaagggctg ccgatggcgc atgacacact cgggactcac ctctggggcc 950
 atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000
 ctgcaggccg atgtctcat cagccaggca gcagccaaaa tctgcgatca 1050
 ccagccaggg gcagccgtct gggaaggagc aagcaaagtg accatttctc 1100
 ctcccctcct tccctctgag aggcctcct atgtccctac taaagccacc 1150
 agcaagacat agctgacagg ggctaattgc tcagtgttgg ccagggaggt 1200
 cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacacggaaa 1250

tgctccagt aagcacaggc tgcaaatcc ccaggcaaag gactgtgtgg 1300
 ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaagg 1350
 agctagagct tggttcaa at gatctccaag ggcccttata cccaggaga 1400
 ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccagggtgcat 1450
 taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacattttgg 1500
 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550
 gccaacatgg tgaaaccct gtctctacta aaaatacaaa aaaactagcc 1600
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 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
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<210> 304
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 304
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 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
 65 70 75
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
 80 85 90
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
 95 100 105
 Arg Arg Arg Asp

<210> 305
 <211> 989
 <212> DNA
 <213> Homo sapiens

<400> 305

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 caccttggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900
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 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306
 <211> 262
 <212> PRT
 <213> Homo sapiens

<400> 306
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 Leu Gly Ser Ala Ala Leu Gly Ala Ala Phe Ala Thr Gly Leu Phe
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 Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Cys
 35 40 45
 Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser
 50 55 60

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
 65 70 75
 Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
 80 85 90
 Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
 95 100 105
 Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
 110 115 120
 Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
 125 130 135
 Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
 140 145 150
 Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
 155 160 165
 Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
 170 175 180
 Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
 185 190 195
 Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
 200 205 210
 Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
 215 220 225
 Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
 230 235 240
 Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
 245 250 255
 Leu Thr Leu Ala Phe Lys Ile
 260

<210> 307
 <211> 2272
 <212> DNA
 <213> Homo sapiens

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 ctctcgccgt cagcatgccca caccgcttca agcccgggga cttggtgttc 100
 gctaagatga agggctaccc tcaactggcct gccaggatcg acgacatcgc 150
 ggatggcgcc gtgaagcccc caccacaaca gtaccccatc tttttctttg 200
 gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

aaatgtaaag acaagtacgg gaagcccaac aagaggaaaag gcttcaatga 300
 agggctgtgg gagatccaga acaacccccca cgccagctac agcgcccctc 350
 cgccagttag ctctccgac agcgaggccc ccgaggccaa ccccgccgac 400
 ggcagttagc ctgacgagga cgatgaggac cgggggggtca tggccgtcac 450
 agcggtaacc gccacagctg ccagcgacag gatggagagc gactcagact 500
 cagacaagag tagcgacaac agtggcctga agaggaaagc gcctgcgcta 550
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 cggagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggtc 700
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 gtcagcctcc gactccgact ccaaggccga ttcggacggg gccaaagcctg 800
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 tctccgact ccgatgtgtc tgtgaagaag cctccgaggg gcaggaagcc 900
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 ggctccgctc cagctccagc agtgacagtg acagcgacga ggtggaccgc 1000
 atcagttagt ggaagcggcg ggacgaggcg cggaggcgcg agctggaggc 1050
 ccggcggcgg cgagagcagg aggaggagct gcggcgccctg cgggagcagg 1100
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 cctctgactc cgagcccagag gccgagctgg agagagaggc caagaaatca 1300
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 gaaggagaag agagtgcggc ccgaggagaa gcaacaagcc aagcccgtga 1400
 aggtggagcg gacccggaag cggctccgagg gcttctcgat ggacaggaag 1450
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 ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttcgccgtta 1650
 caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tatacccggc 1700

tcaagtcgcg ggtcctcggc ccaaagatcg aggcggtgca gaaagtgaac 1750
aaggctggga tggagaagga gaaggccgag gagaagctgg ccggggagga 1800
gctggccggg gaggaggccc cccaggagaa ggcggaggac aagcccagca 1850
ccgatctctc agccccagtg aatggcgagg ccacatcaca gaagggggag 1900
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aaggtgtggc tcctctgaag acctgcacga cagcgtacgg gaggggtccc 2000
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gcagagcaga gaactgtggg gaacgctgtg ctgtttgtat ttgttccctt 2200
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actataaacg gttttttaat ga 2272

<210> 308
<211> 671
<212> PRT
<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met
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Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
				20					25					30
Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
				35					40					45
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
				50					55					60
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
				65					70					75
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
				80					85					90
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
				95					100					105
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
				110					115					120
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
				125					130					135
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser

140 145 150
 Asp Asn Ser Gly Leu Lys Arg Lys Thr Pro Ala Leu Lys Met Ser
 155 160 165
 Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala
 170 175 180
 Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu
 185 190 195
 Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala
 200 205 210
 Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys
 215 220 225
 Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser
 230 235 240
 Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser
 245 250 255
 Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val
 260 265 270
 Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro
 275 280 285
 Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser
 290 295 300
 Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu
 305 310 315
 Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg Glu Leu Glu Ala Arg
 320 325 330
 Arg Arg Arg Glu Gln Glu Glu Glu Leu Arg Arg Leu Arg Glu Gln
 335 340 345
 Glu Lys Glu Glu Lys Glu Arg Arg Arg Glu Arg Ala Asp Arg Gly
 350 355 360
 Glu Ala Glu Arg Gly Ser Gly Gly Ser Ser Gly Asp Glu Leu Arg
 365 370 375
 Glu Asp Asp Glu Pro Val Lys Lys Arg Gly Arg Lys Gly Arg Gly
 380 385 390
 Arg Gly Pro Pro Ser Ser Ser Asp Ser Glu Pro Glu Ala Glu Leu
 395 400 405
 Glu Arg Glu Ala Lys Lys Ser Ala Lys Lys Pro Gln Ser Ser Ser
 410 415 420
 Thr Glu Pro Ala Arg Lys Pro Gly Gln Lys Glu Lys Arg Val Arg
 425 430 435

Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
 440 445 450
 Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys
 455 460 465
 Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
 470 475 480
 Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
 485 490 495
 Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
 500 505 510
 Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys
 515 520 525
 Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala
 530 535 540
 Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
 545 550 555
 Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys
 560 565 570
 Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala
 575 580 585
 Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala
 590 595 600
 Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu
 605 610 615
 Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg
 620 625 630
 Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro
 635 640 645
 Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala
 650 655 660
 Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser
 665 670

<210> 309
 <211> 3871
 <212> DNA
 <213> Homo sapiens

<400> 309
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ttcatcatga atgctaataa agatgaaaga cttaaagcca gaagccaaga 150
 ttttcacctt tttcctgctt tgatgatgct aagcatgacc atgttggtttc 200
 ttccagtcac tggcactttg aagcaaaata ttccaagact caagctaacc 250
 taaaaagact tgctgctttc aaatagctgt attccctttt tgggttcac 300
 agaaggactg gattttcaaa ctcttctctt agatgaggaa agaggcaggc 350
 tgctcttggg agccaaagac cacatctttc tactcagtct ggttgactta 400
 aaaaaaatt ttaagaagat ttattggcct gctgcaaagg aacgggtgga 450
 attatgtaaa ttagctggga aagatgcaa tacagaatgt gcaaatttca 500
 tcagagtact tcagccctat aaaaaactc acatatatgt gtgtggaact 550
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 tcactcctgg agaattgtat aggaatttgg agaggtgcat tatttctttc 3000

B1

tggccactgg gggttaaattt agtgtactac aacattgatt tactgaaggg 3050
 cactaatggtt tccccagga tttctattga ctagtcagga gtaacagggt 3100
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 ataaataagc ctgctacatg t 3871

<210> 310
 <211> 777
 <212> PRT
 <213> Homo sapiens

<400> 310
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 20 25 30
 Phe Leu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Leu
 35 40 45
 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
 50 55 60
 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
 65 70 75
 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

	80		85		90
Phe Leu Leu Ser	Leu Val Asp Leu Asn	Lys Asn Phe Lys Lys	Ile		
	95		100		105
Tyr Trp Pro Ala	Ala Lys Glu Arg Val	Glu Leu Cys Lys Leu	Ala		
	110		115		120
Gly Lys Asp Ala	Asn Thr Glu Cys Ala	Asn Phe Ile Arg Val	Leu		
	125		130		135
Gln Pro Tyr Asn	Lys Thr His Ile Tyr	Val Cys Gly Thr Gly	Ala		
	140		145		150
Phe His Pro Ile	Cys Gly Tyr Ile Asp	Leu Gly Val Tyr Lys	Glu		
	155		160		165
Asp Ile Ile Phe	Lys Leu Asp Thr His	Asn Leu Glu Ser Gly	Arg		
	170		175		180
Leu Lys Cys Pro	Phe Asp Pro Gln Gln	Pro Phe Ala Ser Val	Met		
	185		190		195
Thr Asp Glu Tyr	Leu Tyr Ser Gly Thr	Ala Ser Asp Phe Leu	Gly		
	200		205		210
Lys Asp Thr Ala	Phe Thr Arg Ser Leu	Gly Pro Thr His Asp	His		
	215		220		225
His Tyr Ile Arg	Thr Asp Ile Ser Glu	His Tyr Trp Leu Asn	Gly		
	230		235		240
Ala Lys Phe Ile	Gly Thr Phe Phe Ile	Pro Asp Thr Tyr Asn	Pro		
	245		250		255
Asp Asp Asp Lys	Ile Tyr Phe Phe Phe	Arg Glu Ser Ser Gln	Glu		
	260		265		270
Gly Ser Thr Ser	Asp Lys Thr Ile Leu	Ser Arg Val Gly Arg	Val		
	275		280		285
Cys Lys Asn Asp	Val Gly Gly Gln Arg	Ser Leu Ile Asn Lys	Trp		
	290		295		300
Thr Thr Phe Leu	Lys Ala Arg Leu Ile	Cys Ser Ile Pro Gly	Ser		
	305		310		315
Asp Gly Ala Asp	Thr Tyr Phe Asp Glu	Leu Gln Asp Ile Tyr	Leu		
	320		325		330
Leu Pro Thr Arg	Asp Glu Arg Asn Pro	Val Val Tyr Gly Val	Phe		
	335		340		345
Thr Thr Thr Ser	Ser Ile Phe Lys Gly	Ser Ala Val Cys Val	Tyr		
	350		355		360
Ser Met Ala Asp	Ile Arg Ala Val Phe	Asn Gly Pro Tyr Ala	His		
	365		370		375

300

B1

Lys Glu Ser Ala Asp His Arg Trp Val Gln Tyr Asp Gly Arg Ile
 380 385 390
 Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys Thr Tyr Asp Pro
 395 400 405
 Leu Ile Lys Ser Thr Arg Asp Phe Pro Asp Asp Val Ile Ser Phe
 410 415 420
 Ile Lys Arg His Ser Val Met Tyr Lys Ser Val Tyr Pro Val Ala
 425 430 435
 Gly Gly Pro Thr Phe Lys Arg Ile Asn Val Asp Tyr Arg Leu Thr
 440 445 450
 Gln Ile Val Val Asp His Val Ile Ala Glu Asp Gly Gln Tyr Asp
 455 460 465
 Val Met Phe Leu Gly Thr Asp Ile Gly Thr Val Leu Lys Val Val
 470 475 480
 Ser Ile Ser Lys Glu Lys Trp Asn Met Glu Glu Val Val Leu Glu
 485 490 495
 Glu Leu Gln Ile Phe Lys His Ser Ser Ile Ile Leu Asn Met Glu
 500 505 510
 Leu Ser Leu Lys Gln Gln Gln Leu Tyr Ile Gly Ser Arg Asp Gly
 515 520 525
 Leu Val Gln Leu Ser Leu His Arg Cys Asp Thr Tyr Gly Lys Ala
 530 535 540
 Cys Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp
 545 550 555
 Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala
 560 565 570
 Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp
 575 580 585
 Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val
 590 595 600
 Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro
 605 610 615
 Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly
 620 625 630
 Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys
 635 640 645
 Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser
 650 655 660
 Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr

	665		670		675
Ile Val Lys Leu Thr Leu Asn Val Ile	Glu Asn Glu Gln Met Glu				
680	685			690	
Asn Thr Gln Arg Ala Glu His Glu Glu	Gly Gln Val Lys Asp Leu				
695	700			705	
Leu Ala Glu Ser Arg Leu Arg Tyr Lys	Asp Tyr Ile Gln Ile Leu				
710	715			720	
Ser Ser Pro Asn Phe Ser Leu Asp Gln	Tyr Cys Glu Gln Met Trp				
725	730			735	
His Arg Glu Lys Arg Arg Gln Arg Asn	Lys Gly Gly Pro Lys Trp				
740	745			750	
Lys His Met Gln Glu Met Lys Lys Lys	Arg Asn Arg Arg His His				
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Arg Asp Leu Asp Glu Leu Pro Arg Ala	Val Ala Thr				
770	775				

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 <213> Artificial

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 <223> Synthetic construct.

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 <211> 24
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 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 312
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 <211> 45
 <212> DNA
 <213> Artificial

<220>
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 <223> Synthetic construct.

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<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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 20 25 30
 Gln Arg Leu Glu Gln Arg Arg Gln Gln Ala Ser Glu Arg Glu Ala
 35 40 45
 Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg
 50 55 60
 Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu
 65 70 75
 Leu Gln Gly Ala Gly Leu Asp Val Glu Arg Trp Leu Lys Pro Ala
 80 85 90
 Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser
 95 100 105
 Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp
 110 115 120
 Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu
 125 130 135
 Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro
 140 145 150
 Cys Pro Ala His Val Val Phe Arg Tyr Gln Ala Gly Arg Glu Asp
 155 160 165
 Glu Leu Thr Ile Thr Glu Gly Glu Trp Leu Glu Val Ile Glu Glu
 170 175 180
 Gly Asp Ala Asp Glu Trp Val Lys Ala Arg Asn Gln His Gly Glu
 185 190 195
 Val Gly Phe Val Pro Glu Arg Tyr Leu Asn Phe Pro Asp Leu Ser
 200 205 210
 Leu Pro Glu Ser Ser Gln Asp Ser Asp Asn Pro Cys Gly Ala Glu
 215 220 225
 Pro Thr Ala Phe Leu Ala Gln Ala Leu Tyr Ser Tyr Thr Gly Gln
 230 235 240
 Ser Ala Glu Glu Leu Ser Phe Pro Glu Gly Ala Leu Ile Arg Leu
 245 250 255
 Leu Pro Arg Ala Gln Asp Gly Val Asp Asp Gly Phe Trp Arg Gly
 260 265 270
 Glu Phe Gly Gly Arg Val Gly Val Phe Pro Ser Leu Leu Val Glu
 275 280 285
 Glu Leu Leu Gly Pro Pro Gly Pro Pro Glu Leu Ser Asp Pro Glu
 290 295 300
 Gln Met Leu Pro Ser Pro Ser Pro Pro Ser Phe Ser Pro Pro Ala

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Pro Thr Ser Val	Leu Asp Gly Pro Pro	Ala Pro Val Leu Pro	Gly		
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Asp Lys Ala Leu	Asp Phe Pro Gly Phe	Leu Asp Met Met Ala	Pro		
	335		340		345
Arg Leu Arg Pro	Met Arg Pro Pro Pro	Pro Pro Pro Ala Lys	Ala		
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Pro Asp Pro Gly	His Pro Asp Pro Leu	Thr			
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 <211> 4407
 <212> DNA
 <213> Homo sapiens

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<211> 837
<212> PRT
<213> Homo sapiens

<400> 317

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Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	35	40	45		
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu	50	55	60	
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser	65	70	75	
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu	80	85	90	
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu	95	100	105	
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly	110	115	120	
Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp	125	130	135	
Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu				

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 Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile
 170 175 180
 Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn
 185 190 195
 Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala
 200 205 210
 Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val
 215 220 225
 Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg
 230 235 240
 Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His
 245 250 255
 Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val
 260 265 270
 Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala
 275 280 285
 Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn
 290 295 300
 Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu
 305 310 315
 Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu
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 Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys
 335 340 345
 Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala
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 His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys
 365 370 375
 Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val
 380 385 390
 Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser
 395 400 405
 Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr
 410 415 420
 Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro
 425 430 435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln
 440 445 450
 Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro
 455 460 465
 Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala
 470 475 480
 Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys
 485 490 495
 Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp
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 Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly
 545 550 555
 Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn
 560 565 570
 Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu
 575 580 585
 Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe
 590 595 600
 Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro
 605 610 615
 Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr
 620 625 630
 Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser
 635 640 645
 Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala
 650 655 660
 Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys
 665 670 675
 Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly
 680 685 690
 Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile
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 Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser

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<211> 1197
<212> DNA
<213> Homo sapiens

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<400> 321
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gggattgaac aaaatgaaca gtgggtggc cctcaagtga aagtagagaa 750
gaccgcac gccagacaag caagtgagga agaacttcca ataatgact 800
atactgaaaa tggaaatagaa tttgatccca tgctggaatga gagagggtat 850
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acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950
tcatctgtcg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000
gggagggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050
atataataaa tgcattgctat tcaatgaatt tctgcctatg aggcattctg 1100
cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150
tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaa 1197

<210> 322

<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322

Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu
 1 5 10 15
 Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys
 20 25 30
 Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val
 35 40 45
 Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys
 50 55 60
 Ala Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys
 65 70 75
 Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe
 80 85 90
 Arg Ser Gly Asn Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe
 95 100 105
 Lys Asn Gly Tyr Thr Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys
 110 115 120
 Phe Ile Lys Thr Gln Ile Lys Val Ile Pro Glu Phe Ser Glu Pro
 125 130 135
 Glu Glu Glu Ile Asp Glu Asn Glu Glu Ile Thr Thr Thr Phe Phe
 140 145 150
 Glu Gln Ser Val Ile Trp Val Pro Ala Glu Lys Pro Ile Glu Asn
 155 160 165
 Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu Ile Cys Asp Asn
 170 175 180
 Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser Val Ser Glu
 185 190 195
 Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe Pro Ala
 200 205 210
 Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val Pro
 215 220 225
 Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu
 230 235 240
 Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe
 245 250 255
 Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg
 260 265 270

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
 275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
 290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
 305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

gcggaactgg ctccggctgg cacctgagga gcggcgtgac cccgagggcc 50
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 ggccgtgcag cttctgggct tctgtctcag cttcctgggc atggtgggca 150
 cgttgatcac caccatcctg ccgcaactgg ggaggacagc gcacgtgggc 200
 accaacaatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250
 tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300
 tggcgtgcc ccaagacctc caggctgccc gcgccctcat ggtcatctcc 350
 tgccctgctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400
 cacgcgtgc gccaaagggca caccgcgcaa gaccaccttt gccatcctcg 450
 gcggcacccct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500
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 cggcatgaag tttgagattg gccaggccct gtacctgggc ttcattctct 600
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 tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850
 gtccccggcg ggactgtcaa tggaggcagg ggttccagca caaagtttac 900
 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaaatgt 950
 ctttagagca cagggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
 atatttatgt ggggtgattg ataacaagtt taatataaag tgacttggga 1100
 gtttggtcag tggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324
 <211> 239
 <212> PRT
 <213> Homo sapiens

<400> 324

Met Ala Ser Thr Ala Val Gln Leu Leu Gly Phe Leu Leu Ser Phe
 1 5 10 15
 Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp
 20 25 30
 Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser
 35 40 45
 Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
 50 55 60
 Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln
 65 70 75
 Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
 80 85 90
 Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
 110 115 120
 Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala
 125 130 135
 Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro
 140 145 150
 Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr
 155 160 165
 Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu
 170 175 180
 Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln
 185 190 195
 Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala
 200 205 210
 Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val
 215 220 225

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
 gagctcccct caggagcgcg ttagcttcac accttcggca gcaggagggc 50
 ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100
 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150
 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200
 aaccccgta cctccgtgtt ccagtagcaa gggctctgga ggagctgcgt 250
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
 gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcata 350
 gtcttggtg ccattggcct cctggtatcc atctttgccc tgaaatgcat 400
 ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450
 ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500
 gtgtttgcca acatgctggg gactaacttc tggatgtcca cagctaacaat 550
 gtacaccggc atgggtggga tgggtgcagac tggtcagacc aggtacacat 600
 ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
 gggggtgtga tgatgtgcat cgctgcccgg ggcctggcac cagaagaaac 700
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
 aagaagatat acgatggagg tgccgcaca gaggacgagg tacaatctta 850
 tccttccaag cagactatg tgtaatgctc taagacctct cagcacgggc 900
 ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950
 atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150
 gagaatgtgg tttaaatctc tctctcacat tttgatgatt tagacagact 1200
 cccctcttc ctctagtca ataaacccat tgatgatcta tttcccagct 1250

tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300
 ttctgctggt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350
 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
 cccatgatct cggttttctt acaactgtgat cttaaaagtt accaaaccaa 1450
 agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500
 tcttattaca gcaacaccat tctaggagtt tcctgagctc tccactggag 1550
 tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
 taaaatgata cactatctct gtgaaatagc ctcaccccta catgtggata 1700
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcacttttg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
 gaggctgagg tgggaggatc acttgagccc agggagggtg gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaac taattcttta a 2121

<210> 326
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
1				5					10					15
Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly

80 85 90

Ala Ile Gly Leu Leu Val Ser Ile Phe Ala Leu Lys Cys Ile Arg
 95 100 105

Ile Gly Ser Met Glu Asp Ser Ala Lys Ala Asn Met Thr Leu Thr
 110 115 120

Ser Gly Ile Met Phe Ile Val Ser Gly Leu Cys Ala Ile Ala Gly
 125 130 135

Val Ser Val Phe Ala Asn Met Leu Val Thr Asn Phe Trp Met Ser
 140 145 150

Thr Ala Asn Met Tyr Thr Gly Met Gly Gly Met Val Gln Thr Val
 155 160 165

B1 Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe Val Gly Trp Val
 170 175 180

Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met Cys Ile Ala
 185 190 195

Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala Val Ser
 200 205 210

Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly Phe
 215 220 225

Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
 230 235 240

Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro
 245 250 255

Ser Lys His Asp Tyr Val
 260

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
 ggaaaaactg ttctcttctg tggcacagag aaccctgctt caaagcagaa 50
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 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgcggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgetgtctcc gtgatgtcct tcttggtctt catgatggcc atccttggca 400
 tgaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450
 ctgtgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgcgt 650
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atcgcacaa ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tactttctca aaatggaccc 850
 caaagaaact ttgatttact gttcttaact gcctaactct aattacagga 900
 actgtgcatc agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaaacc aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taaggtgggt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattatct tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgtg acatttatat ctacataga gacatgctta 1150
 tatgggtttt tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgcttttcag ggaaatcatg gatagggttg aagaagggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400
 atcctcttct ccagaggct tttttttct tgtgtattaa attaacattt 1450
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550
 gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgaggttt catcaatata aataaaagag cagaaaaata 1700
 tgtcttggtt ttcatttgct taccaaaaaa acaacaaca aaaaagttgt 1750
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

B1

atttttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgttttag 1850
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
 aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000
 ttttctaatt 2010

<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328

Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly
 1 5 10 15
 Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp
 20 25 30
 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
 35 40 45
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
 50 55 60
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
 65 70 75
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
 80 85 90
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
 110 115 120
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
 125 130 135
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
 140 145 150
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
 155 160 165
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
 170 175 180
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
 185 190 195
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
 200 205 210

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215				220					225	

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329

tcgccaatggc ctctgccgga atgcagatcc tgggagtcgt cctgacactg 50
 ctgggctggg tgaatggcct ggtctcctgt gccctgccca tgtggaaggt 100
 gaccgctttc atcggcaaca gcatcgtggt ggcccagggtg gtgtgggagg 150
 gcctgtggat gtcctgcgtg gtgcagagca ccggccagat gcagtgaag 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300
 ttgctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
 cgctgtgtgc tcacctctgg gattgtcttt gtcattctcag gggtcctgac 400
 gctaataccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
 accccctggt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
 ttgggctggg cggcctcagg ccttttgttg ctgggtgggg ggttgctgtg 550
 ctgcacttgc cctcggggg ggtcccaggg cccagccat tacatggccc 600
 gctactcaac atctgccct gccatctctc gggggccctc tgagtaccct 650
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
 gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750
 ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
 gctgtttctc acccttgat gatggagcca aagaggggat gctttgagat 900
 tctggatctt gacatgccca tcttagaagc cagtcaagct atggaactaa 950
 tgcggaggct gcttgctgtg ctggctttgc aacaagacag actgtcccca 1000
 agagttcctg ctgctgctgg gggctgggct tccctagatg tactggaca 1050
 gctgcccccc atcctactca ggtctctgga gtcctctct tcaccctgg 1100
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
 cctctgtttc ctccgtcctg ataagacgtc cccccccag ggccagggtcc 1200
 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgcct 1250

gccccctcg tctaccccc ttacactca catttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu
1 5 10 15

Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp
20 25 30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
35 40 45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
50 55 60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
80 85 90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
95 100 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
110 115 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
125 130 135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
140 145 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
155 160 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu
170 175 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
185 190 195

Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
200 205 210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
215 220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100
gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150
gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtgg 200
ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300
gcaagttcta tagctccttg ttggctctcc cgctgcccct ggaaacagcc 350
cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccctgcttat 400
tggcatctgt ggcataagc aggtccagtg cacaggctct aacgagaggg 450
ccaaagcata ctttctggga acttcaggag tcctcttcat cctgacgggt 500
atcttcgttc tgattccggt gagctggaca gccaatataa tcatcagaga 550
tttctacaac ccagccatcc acataggta gaaacgagag ctgggagcag 600
cacttttctt tggctgggca agcgtgctg tcctcttcat tggagggggg 650
ctgctttgtg gattttgtg ctgcaacaga aagaagcaag ggtacagata 700
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
caatgcttag taagacctcc accagttagt tctaagcct ccttttggct 800
ccaagtatgg actatggtca atgtttttta taaagtcctg ctagaaactg 850
taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900
cgaaagtttc aatttggtac tgggtgtagg aatgaaaatg acttacttgg 950
acattctgac ttcaggtgta ttaaagcat tgactattgt tggacccaat 1000
cgctgctcca attttcatat tctaaattca agtataacca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100
ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150
acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1 5 10 15
 Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg
 20 25 30
 Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu
 35 40 45
 Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn
 50 55 60
 Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe
 65 70 75
 Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala
 80 85 90
 Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly
 95 100 105
 Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser
 110 115 120
 Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys
 125 130 135
 Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly
 140 145 150
 Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu
 155 160 165
 Ser Lys Thr Ser Thr Ser Tyr Val
 170

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
 agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50
 atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100
 ctcagaagct gctagtctgt ctcaaaaaa agtggactgc agcatttaca 150
 agaagtatcc agtgggtggc atcccctgcc ccatcacata cctaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
 ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

cccgcgcccc gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50

ctgctcgcgc cccgcgcgca tggctgcctc ccccgcgcgg cctgctgtcc 100

tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaatt 550

agcgattctc ttcattgtatc tcctaattgcc ttacactact tggttttctga 600

tttgccttat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
 gaagagttaa aacaacacat gtaaagcct tttgatattt catgggaatg 700
 cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 336
 Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
 1 5 10 15
 Leu Ala Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
 20 25 30
 Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
 35 40 45
 Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
 50 55 60
 Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
 65 70 75
 Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
 80 85 90
 Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
 95 100 105
 Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
 110 115 120
 Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
 125 130 135
 Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
 140 145

<210> 337
 <211> 1310
 <212> DNA
 <213> Homo sapiens

<400> 337
 cggctcgagc ccgcccggaa gtgcccagg ggccgcgatg gagctggggg 50
 agccgggagc tcggtagcgc ggcgggcaag gcaggcgcca tgaccctgat 100
 tgaaggggtg ggtgatgagg tgaccgtcct tttctcgggtg cttgcctgcc 150
 ttctggtgct ggcccttgcc tgggtctcaa cgacacccgc tgagggcggg 200
 gaccactgc ccagccgctc agggacccca acgcatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300
 cccccagcct gagacacaga ggtcaagctg cacagccaga gcccagcacg 350
 gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400
 gctacggctg aaattcctca atgattcaga gcagggtggcc agggcctggc 450
 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
 cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
 gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
 tgtccacgag agtcggtccc ccaaattccc cctgcccgcc ggggtccgag 650
 cccggcccct cggggctgga aatcggcagc ctgctgctgc ccctgctgct 700
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
 ttcccctgac cgccactctg ggccctggccg gcttcaccct gctcctcagt 800
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 ctgcctgccc agggccgcct ctccggcctg cctcttcccg ctgccctgga 950
 gcccagccct gcgccgcaga ggactcccgg gactggcgga ggccccgccc 1000
 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
 cgcactggga gtgggctcct cggggctcggg catctgctgt cgctgcctcg 1100
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 acgccaggtc ggtgggaggc tggggaaggg gagcggggag gggcagagga 1250
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 aaaaaaaaaa 1310

<210> 338
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 338
 Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
 1 5 10 15
 Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
 20 25 30
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
 35 40 45

Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp
 50 55 60
 Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg
 65 70 75
 His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr
 80 85 90
 Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu
 95 100 105
 Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp
 110 115 120
 Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly
 125 130 135
 Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly
 140 145 150
 Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys
 155 160 165
 Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro
 170 175 180
 Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile
 185 190 195
 Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu
 200 205 210
 Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala
 215 220 225
 Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala
 230 235 240
 Phe Ala Met Tyr Arg Pro
 245

<210> 339
 <211> 849
 <212> DNA
 <213> Homo sapiens

<400> 339
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 tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100
 caagacccta agaaccatca gccctcagct gcacctctc ccctccaagg 150
 atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200
 tcaggccagc ctcacagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttgga tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300
 gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
 tggaagcttt gactatggcc tcttccagat caacagccac tactgggtgca 400
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
 ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
 gtccggagca cgggggatga acaactgggt agaattggagg ttgcactgtt 550
 caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600
 aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650
 ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700
 ccttcccatt tacaactaaa actgaccaga gcccagga taaatggttt 750
 tcttggttc ctccttactc ccatctggac ccagtcccct gggtcctgtc 800
 tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 340

Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala
 1 5 10 15
 Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val
 20 25 30
 Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
 35 40 45
 Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
 50 55 60
 Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
 65 70 75
 Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
 80 85 90
 Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
 95 100 105
 Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
 110 115 120
 Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
 125 130 135
 Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

<210> 341
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 341
ccctccaagg atgacaaagg cgc 23

<210> 342
<211> 29
<212> DNA
<213> Artificial

B1
<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.

<400> 342
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 343
atctcaggcg gcatcctgtc agcc 24

<210> 344
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 344
gtggatgcct gcaagaaggt tggg 24

<210> 345
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

B1
<400> 346
tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50
actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100
caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150
aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtcctt 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350
aaacttccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400
gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttgga 450
gttctagcaa catgtccta aggaagcgat acaggcacag accatgcaga 500
ctccagttcc tctgctgct cctgatgctg ggatgcgtcc tgatgatggt 550
ggcgatgttg caccctcccc accacaccct gcaccagact gtcacagccc 600
aagccagcaa gcacagccct gaagccaggt accgcctgga ctttggggaa 650
tcccaggatt ggggtactgga agctgaggat gaggggtgaag agtacagccc 700
tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750
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ggtgggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850
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 aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900
 gggttgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950
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 gagaaaaaag ctctatgaaa gaatatagga agtttctcct tttcacacct 2550

B1

tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln
1 5 10 15

Phe Leu Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val
20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Gly Ser Tyr Arg Leu Ile
110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Glu Leu Thr
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
245 250 255

Arg Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly
 260 265 270
 Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His
 275 280 285
 Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile
 290 295 300
 Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile
 305 310 315
 Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg
 320 325 330
 Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro
 335 340 345
 Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg
 350 355 360
 Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr
 365 370 375
 Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly
 380 385 390
 Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly
 395 400 405
 Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln
 410 415 420
 Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg
 425 430 435
 Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu
 440 445 450
 Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala
 455 460 465
 Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu
 470 475 480
 Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu
 485 490 495
 Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His
 500 505 510
 Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp
 515 520 525
 Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg
 530 535 540
 Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe

	545		550		555
Gly Ser Pro Gln	His Leu Cys Phe Ala	Val Arg Gln Glu Gln	Val		
	560		565		570
Ile Leu Gln Asn	Cys Thr Glu Glu Gly	Leu Ala Ile His Gln	Gln		
	575		580		585
His Trp Asp Phe	Gln Glu Asn Gly Met	Ile Val His Ile Leu	Ser		
	590		595		600
Gly Lys Cys Met	Glu Ala Val Val Gln	Glu Asn Asn Lys Asp	Leu		
	605		610		615
Tyr Leu Arg Pro	Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg	Phe		
	620		625		630
Asp Gln Ile Asn	Ala Val Asp Glu Arg				
	635				

<210> 348

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 348

ggagaggtgg tggccatgga cag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 350

tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351
 <211> 2524
 <212> DNA
 <213> Homo sapiens

<400> 351
 cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50
 ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100
 tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
 tcttcatacct cccctcgaac cccaccagcc ccagcccgcc ccccggtgtgc 200
 caggggaggg ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250
 ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcctg 300
 cctggcactg cacccccagc caccatca ggctttgagg aggggccgcc 350
 ctcateccaa taccctggg ctatcgtgtg gggcccacc gtgtctcgag 400
 aggatggagg ggacccaac tctgccaatc ccggatttct ggactatggt 450
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 ggccattcct gttcgggggc cgtggggaag gtgtggaccc ccagctctat 600
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 caccctgac catgaggagc cccgaggggg accccggcct gggatgcccc 850
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ccaagcagga ggccaagggg ccggcacagc ccccatccca ctgaggggtgg 1350
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 gggtagtgag gcccagact tcacccccag cccactgcta aaatctgttt 2000
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 actcccattt gcccttccct ttctcttaca gtcccttttg tcttgtctgt 2100
 cctggctgtc tgttgtgtgt ccattctctg gacttcagag cccctgagc 2150
 cagtcctccc ttccagcct ccttttgggc ctccctaact ccacctaggc 2200
 tgccagggac cggagtcagc tggttcaagg ccacgggag ctctgcctcc 2250
 aagtctaccc ttcccttccc ggactccctc ctgtcccctc ctttctctcc 2300
 tccttcttc cactctcctt ccttttgctt cctgcccctt tccccctct 2350
 caggttcttc cctccttctc actgggtttt ccaccttctt ccttcccttc 2400
 ttccctggct cctaggctgt gatatatatt tttgtattat ctctttcttc 2450
 ttcttggtg gatcatcttg aattactgtg ggatgtaagt ttcaaaattt 2500
 tcaaataaag cctttgcaag ataa 2524

<210> 352
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 352
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
 1 5 10 15

Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20 25 30
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
 140 145 150
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
 155 160 165
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
 170 175 180
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
 185 190 195
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
 200 205 210
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
 215 220 225
 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
 230 235 240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

gttaaccagc gcagtcctcc gtgcgtcccg cccgccgctg ccctcactcc 50

cggccaggat ggcacacctgt ctggccctgc gcatggcgct gctgctggtc 100

tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggcccccca 250
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
 ggaccagggc ggcgggtcgc tggggcccg cgctatcgcg gccatcgtga 350
 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 354
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
 1 5 10 15
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
 20 25 30
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120
 Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
 ggccgttggt tgggtgcgcg ctgaagggtg tggcgcgagc agcgtcgttg 50
 gttggccggc ggcgggccgg gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gggcgctgg cccacggctg tctgcactgc cacagcaact 150
 tctccaagaa gttctccttc taccgccacc atgtgaactt caagtcctgg 200
 tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
 cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300
 agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
 taccagggga agatgtactt ccccggtat ttccccaacg agctgcgaaa 400
 catcttcgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450
 acctggcacc aggcagctgg ggaggaggcg agctctccag ggagggaccc 500
 agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550
 agtagcccc agaggcgctg ggagtgttg caccgccctc ccctgaagtt 600
 tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggcc 650
 atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700
 tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750
 acgtcgctg ctttggtat aactgcgagt agggctcagg catcacacc 800
 acccgtgcca gggccctact gtccctgggg tcccaggctc tccttgagg 850
 gggctcccc ccttcacct ggctgtcatc gggtagggcg gggccgtggg 900
 ttcagggcg caccacttc aagcctgtgt cccacaggtc ctcggcgcag 950
 tggaagtcag ctgtccagg cctcctgaac tacataaata actggcacia 1000
 gtaagtcccc tcctcaaacc aacacaggca gtgtgtgtat gtgagcacct 1050
 cgtgggtgag tatgtgtgg gcacaggctg gtcctcag ctcccacgtc 1100
 ctagaggggc tcccaggag gtggaacctc aaccagctc tgcgcaggag 1150
 gcggctgcag tccttttctc cctcaaaggc ctccgacct cagctggagg 1200
 cgggcatctt tcctaaagg tcccatagg gtctggttc acccatccc 1250
 aggtctgtgg tcagagcctg ggagggttc ctacgatgg taggggtgcc 1300
 ccatggagg gctgactgcc ccacattgcc ttccagacag gacacgagca 1350
 tgaggtaagg ccgcctgac ctggacttca gggggagggg gtaaaggag 1400
 agaggaggg ggctagggg tcctctagat cagtgggggc actgcaggtg 1450
 gggctctccc tatacctgg acacctgct gatgtcacct ctgcaaccac 1500
 acccatgtgg tggttcatg aacagaccac gtcctctgc cttctcctgg 1550

B1

cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600
 ggcctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650
 gcacaccctt cggacatccc aggcacgagg gtgtcgtgga tgtggccaca 1700
 cataggacca cacgtcccag ctgggaggag aggcctgggg cccccaggga 1750
 gggaggcagg ggggtgggga catggagagc tgaggcagcc tcgtctcccc 1800
 gcagcctggt atcgccagcc ttaaggtgtc tggagcccc acacttggcc 1850
 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900
 gctgggcctg ccccagggca acgtgggggc ggagactcag ctggacagcc 1950
 cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000
 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggagggagg 2050
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100
 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala	1	5	10	15
His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser	20	25	30	
Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp	35	40	45	
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr	50	55	60	
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu	65	70	75	
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln	80	85	90	
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu	95	100	105	
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala	110	115	120	
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln	125	130	135	
Leu	Ser	Arg	Glu	Gly	Pro	Ser	Leu	Ala	Pro	Glu	Gly	Ser	Met	Pro				

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

agcaggagca ggagagggac aatggaagct gccccgtcca gggtcatgtt 50
cctcttattt ctcctcacgt gtgagctggc tgcagaagtt gctgcagaag 100
ttgagaaatc ctcagatggc cctgggtgctg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgccc atactccata 250
gcatggtgca aaaattccca ggctgtgcat ttgggatcag cactgattct 300
gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
tcagattcat ctcctcctga taatgaacaa ggctcccca gagtatgaag 550
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctctttattc tgggtggacag tggatatgaaa gaaaatggga aggtgatatc 650
atctttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700
ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750
catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
aactcaaate tcagagacac taaacaacag gatcactagg cctgccaacc 950
acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
tctcttcttc cttcttttaa atttcatatc ctcactccct atccaatttc 1100
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
tcaaaaacca aaggatggtt ttaaacacct ttgtgaaatt gtctttttgc 1400
cagaagttaa aggctgtctc caagtcctcg aactcagcag aaatagacca 1450
tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaatcaa 1500
caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358
<211> 273
<212> PRT
<213> Homo sapiens

B1
<400> 358
Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu
1 5 10 15
Thr Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser
20 25 30
Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp
35 40 45
Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val
50 55 60
Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu
65 70 75
His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser
80 85 90
Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr
95 100 105
Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu
110 115 120
Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe
125 130 135
Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val
140 145 150
Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu
155 160 165
Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His
170 175 180
Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe
185 190 195

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

B1

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 359
 ccagcagtgcc ccatctcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

B1
<400> 363
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
ccggcgcggg tggcgagag atcagaagcc tcttcccaa gccgagccaa 100
cctcagcggg gaccgggct caggacgcg gcggcgcgcg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggtcggg gctggcgcg gcgcttgggc 250
tcttgacagc tggagtatca gccttgaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcgggttga cctcagtcct ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg ttttccact actccaagg gcaagtgtac 450
cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgaçat cgttgtccag 600
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgttt 650
tccagtttgg gtagtggtgg gcatagttac tgctgtgggc ctaggtctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggtcct gtaaagagtc 850
tgcttcttgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatatc cgaaagaatt aagagaatac ctagaacata tctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050
 atgtagcctt ggagacccag gcaaggacaa gtacacgtgt actcacagag 1100
 ggagagaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150
 cctgatatga ggagccagtg ttgcatgatg aaaagatggt atgattctac 1200
 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250
 caattgggag atttcagaaa cattcctttc accatcattt agaaatggtt 1300
 tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350
 ccttttaatc taagggctta agactgatta gtcttagcat ttactgtagt 1400
 tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450
 cagtatcagt accattttatt tgtctgccgc ttttaaaaaa taccattgg 1500
 ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600
 tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
 attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364
 <211> 269
 <212> PRT
 <213> Homo sapiens

<400> 364
 Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
 1 5 10 15
 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
 20 25 30
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
 35 40 45
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
 50 55 60
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
 65 70 75
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
 80 85 90
 Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
 95 100 105

Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile
 110 115 120
 Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys
 125 130 135
 Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile
 140 145 150
 Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val
 155 160 165
 Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr
 170 175 180
 Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn
 185 190 195
 Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser
 200 205 210
 Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly
 215 220 225
 Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile
 230 235 240
 Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile
 245 250 255
 Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn
 260 265

<210> 365
 <211> 1321
 <212> DNA
 <213> Homo sapiens

<400> 365
 gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50
 cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggg 100
 ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
 aggggcgcgg ccccgccgca gtccccgcg gcccccgacc ctgaggcgtc 250
 gcctctggcc gagccgccac aggagcagtc cctcgccccg tgggtctccgc 300
 agaccccggc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350
 agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400
 agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450
 gttatgctga tgttgagaac cgtgtacat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650
 agattactga tttcccatTT aagtgggaatt cgtcattatg aaaaggacat 700
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850
 ttcaaaacct ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
 caggaagaaa acgagccagt gatttacaat agagcaaggt aaatgaatac 1150
 cttctgctgt gtctagctat atcgcatctt aacactatTT tattaattaa 1200
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

<210> 366
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5					10					15
Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20					25					30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35					40					45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50					55					60
Arg	Gly	Ala	Ala	Pro	Ala	Gln	Ser	Pro	Ala	Ala	Pro	Asp	Pro	Glu
				65					70					75
Ala	Ser	Pro	Leu	Ala	Glu	Pro	Pro	Gln	Glu	Gln	Ser	Leu	Ala	Pro
				80					85					90

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala
 95 100 105
 Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp
 110 115 120
 Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly
 125 130 135
 Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn
 140 145 150
 Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile
 155 160 165
 Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala
 170 175 180
 Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu
 185 190 195
 Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr
 200 205 210
 Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys
 215 220 225
 Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys
 230 235 240
 Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys
 245 250 255
 Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu
 260 265 270
 Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn
 275 280 285
 Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn
 290 295 300
 Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe
 305 310 315
 Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu
 320 325 330
 Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
 335 340 345
 Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
 350 355 360
 Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
 365 370

<210> 367

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tggaaaagaa gtctggtcag aaggtttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggctt cattctcctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat ttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat gggtgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150
agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200
tggggcgga ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250
tggagcactc atttgagatc gatgacagt ccaacttccg gaagcggggc 300
tcaactgctc ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350
gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
gaagctggtg gctatgtctc ctctttgtc cctgctgct ccctggtgga 500
gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
tggtgggcgt gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600
gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650
gcccaccaca gcccagggc ctgagacggc ggccttcatt gagcgcctgg 700
agatggaaca ggcccagaag gccaagaacc ccaggagca gaagtccttc 750
ttcgccaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800
gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
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ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
agcttccagc agccaaaagc aactgttggt ttggcaagac ggtcctgatg 1000
tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050
caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctgagctgtg 1100
ttgtgtggca gtttattaaa ctgtccccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10				15	
Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25				30	
Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
			35						40				45	

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe
 50 55 60
 Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu
 65 70 75
 Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu
 80 85 90
 Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn
 95 100 105
 Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp
 110 115 120
 Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys
 125 130 135
 Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val
 140 145 150
 Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro
 155 160 165
 Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu
 170 175 180
 Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
 185 190 195
 Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala
 200 205 210
 Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys
 215 220 225
 Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
 230 235 240
 Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly
 245 250 255
 Gly Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu
 260 265

<210> 373
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 373
 ggagcgtgc tggaaccga gccggagccg gagccacagc ggggaggggtg 50
 gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100
 cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150
 tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200

ctaaaccccc tggaagggcc tgcagcaatc cctccttcct tcggtttcaa 250
 ctggactttct atcaggtcta cttcctggcc ctggcagctg attggcttca 300
 ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
 aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
 ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
 cctctttctcc ctgacttact cactatgctg cttaacaaaa ctctctcaag 500
 actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550
 ctgctcttct cagccttcga ggcctggtat atccatgagc acgtggaacg 600
 gcatgacttc cctgctgagt ggatcccage tacctttgct cgagctgcct 650
 tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
 gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750
 tctcctggct ctggcagggg ccttgggcct tcgaaactgg ggggagaact 800
 atgaccggca gcgctgccttc tcaaggacct gtgctggagg cctgcgctgc 850
 ctctgtcgg accgcccgt gctgctgctg ggcaccatac aagctctatt 900
 tgagagtgtc atcttcatct ttgtcttct ctggacacct gtgctggacc 950
 cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
 ctgcttggt cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
 tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100
 tcttcatggt gactttctct accagcccag gccaggagag tccggtggag 1150
 tccttcatag cttttctact tattgagttg gcttgtggat tatactttcc 1200
 cagcatgagc ttcctacgga gaaaggatgat ccctgagaca gagcaggctg 1250
 gtgtactcaa ctggttccgg gtacctctgc actcactggc ttgcctaggg 1300
 ctcttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatggt 1350
 cagcatttgc tctgctgtca tggatgaggc tctgctggca gtggtgggac 1400
 tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
 gaggagccct atgccctga gctgtaaccc cactccagga caagatagct 1500
 gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
 gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
 gggaggacat gatgggggtg atggactgga aagaagggtgc caaaagttcc 1650

ctctgtgtta ctccattta gaaaataaac actttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
1 5 10 15

Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
20 25 30

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
35 40 45

Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
50 55 60

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
65 70 75

Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
80 85 90

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
95 100 105

Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
110 115 120

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
125 130 135

Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
140 145 150

Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
155 160 165

Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
170 175 180

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
185 190 195

Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
200 205 210

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
215 220 225

Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
230 235 240

Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile
 245 250 255
 Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp
 260 265 270
 Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe
 275 280 285
 Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg
 290 295 300
 Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu
 305 310 315
 Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr
 320 325 330
 Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile
 335 340 345
 Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser
 350 355 360
 Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala
 365 370 375
 Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys
 380 385 390
 Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr
 395 400 405
 Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu
 410 415 420
 Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu
 425 430 435
 Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu
 440 445 450

<210> 375
 <211> 1098
 <212> DNA
 <213> Artificial

<400> 375
 gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50
 gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tcgtgctctg 100
 gctccccgcg tgcgtcgcgg cccacggctt ccgtatccat gattatttgt 150
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
 cctgccaagg actttggtgg tatctttcac acaaggtatg agcagattca 250

ccttgcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
 tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgtccttc 350
 ctctccaaga ctcggtggt ccaggagcac ggcgggcggg cggatgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagtaccca ggcacagct gacatccccg ccctcttctt gctcggccga 500
 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttgagaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
 tttgggcgtt gctaggctga aagggaagcc acaccactgg ccttcccttc 800
 cccagggccc ccaaggtgt ctcatgtac aagaagaggc aagagacagg 850
 cccaggggt tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
 taccaggggt ctctgcacag tgaccttcac agcagttgtt ggagtgggtt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5					10					15

Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20					25					30

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35					40					45

Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
				50					55					60

Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
				65					70					75

Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
				80					85					90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
 95 100 105
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
 110 115 120
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
 125 130 135
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
 140 145 150
 Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
 155 160 165
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
 170 175 180
 Leu Gln Pro Pro Trp Thr Phe Trp
 185

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
 ggctgggtgt gatggctgtg gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caaccctaaag 200
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagaccacgg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val
 1 5 10 15
 Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys
 20 25 30
 Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly
 35 40 45
 Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr
 50 55 60
 Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
 65 70 75
 Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile
 80 85 90
 His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe
 95 100 105
 Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu
 110 115

<210> 379
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 379
 ctgcctccac tgctctgtgc tggg 24

<210> 380
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 380
 cagagcagtg gatgttcccc tggg 24

<210> 381
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ccttctggat gggggcccag gggggccagg agagtataaa 50
ggcgatgtgg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150
ctcctggggg gccccacctg ggcagggaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
ctttcctccg gggatgggtc atgtacacca gcaaggaccg ctatttctat 450
tttggaagc ttgatggcca gatctcctct gcctaccca gccaagaggg 500
gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650
ggtatggggc catccgagct gaggccatct gtgtggtggt ggctgatggt 700
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1				5				10					15	
Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20				25					30	
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
				35				40					45	

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
 50 55 60
 Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
 65 70 75
 Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
 80 85 90
 Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
 95 100 105
 Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
 110 115 120
 Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
 125 130 135
 Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
 140 145 150
 Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
 155 160 165
 Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
 170 175

<210> 384
 <211> 2379
 <212> DNA
 <213> Homo sapiens

<400> 384
 gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50
 agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100
 atacagatgt ggcagctcag gtagcccca attgcctgga agaatacatc 150
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
 cccctcccca ccccccaaaa aaactgtaaa gatgcaaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
 tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
 atgttccaaa atcgggtccat ctccaagggt gtccaatttt tcttcttggg 400
 tgtcagcgag cctgactca ctacagtgc gctgacagg gctgtcatgc 450
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
 acaaaggatg gggttcaatg taattaggct actgagcgga tcagctgtag 550
 cactgggttat agccccact gtcttactga caatgctttc ttctgccgaa 600
 cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tataatctgct gggtgcttag 700
 gtttgctccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
 aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
 gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050
 aacctggaac ttttggacct gggatataac cggatccgaa gtttagccag 1100
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
 atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200
 cagaaccttt acttgcaagt gaataaaatc agtgtcatag gacagaccat 1250
 gtccctggacc tggagctcct taaaaaggct tgatttatca ggcaatgaga 1300
 tcgaagcttt cagtggaccc agtgttttcc agtgtgtccc gaatctgcag 1350
 cgccctcaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400
 ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450
 aatgcagcag aatatattgc tccctgttaa actggctgaa aagttttaaa 1500
 ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
 agtaaagtgt atcgatgcag tgaagaacta cagcatctgt ggcāaaagta 1600
 ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650
 cccaagctcc ccaggccgaa gcatgagagc aaacccccctt tgcccccgac 1700
 ggtgggagcc acagagcccc gccagagac cgatgctgac gccgagcaca 1750
 tctctttcca taaaatcatc gcgggcagcg tggcgctttt cctgtccgtg 1800
 ctgctcatcc tgctggttat ctacgtgtca tggaagcggg accctgagag 1850
 catgaagcag ctgcagcagc gtcctcat gcgaaggcac aggaaaaaga 1900
 aaagacagtc cctaaagcaa atgactccca gcacccagga attttatgta 1950
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
 gggaccctgc acctataaca aatcgggctc cagggagtgt gaggtatgaa 2050
 ccattgtgat aaaaagagct cttaaaagct gggaaataag tgggtgcttta 2100

ttgaactctg gtgactatca aggggaacgcg atgccccccc tcccccttccc 2150
 tctccctctc acttttggtgg caagatcctt ccttggtccgt tttagtgcac 2200
 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385

Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
 1 5 10 15
 Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
 20 25 30
 Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
 35 40 45
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
 50 55 60
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
 65 70 75
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
 80 85 90
 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
 95 100 105
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
 110 115 120
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
 125 130 135
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
 140 145 150
 Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
 155 160 165
 Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
 170 175 180
 Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
 185 190 195
 Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu

200 205 210
 His Leu Glu His Asn Gln Phe Ser Lys Leu Asn Leu Ala Leu Phe
 215 220 225
 Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr Leu Gln Trp Asn Lys
 230 235 240
 Ile Ser Val Ile Gly Gln Thr Met Ser Trp Thr Trp Ser Ser Leu
 245 250 255
 Gln Arg Leu Asp Leu Ser Gly Asn Glu Ile Glu Ala Phe Ser Gly
 260 265 270
 Pro Ser Val Phe Gln Cys Val Pro Asn Leu Gln Arg Leu Asn Leu
 275 280 285
 Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln Glu Ile Leu Asp Ser
 290 295 300
 Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala Gly Asn Ile Trp Glu
 305 310 315
 Cys Ser Arg Asn Ile Cys Ser Leu Val Asn Trp Leu Lys Ser Phe
 320 325 330
 Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys Ala Ser Pro Lys Glu
 335 340 345
 Leu Gln Gly Val Asn Val Ile Asp Ala Val Lys Asn Tyr Ser Ile
 350 355 360
 Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp Leu Ala Arg Ala Leu
 365 370 375
 Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro Arg Pro Lys His Glu
 380 385 390
 Ser Lys Pro Pro Leu Pro Pro Thr Val Gly Ala Thr Glu Pro Gly
 395 400 405
 Pro Glu Thr Asp Ala Asp Ala Glu His Ile Ser Phe His Lys Ile
 410 415 420
 Ile Ala Gly Ser Val Ala Leu Phe Leu Ser Val Leu Val Ile Leu
 425 430 435
 Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys
 440 445 450
 Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys
 455 460 465
 Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr
 470 475 480
 Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu
 485 490 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 386
ctgggatctg aacagtttcg gggc 24

<210> 387
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 387
ggtccccagg acatggtctg tccc 24

<210> 388
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 388
gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
<211> 1449
<212> DNA
<213> Homo sapiens

<400> 389
agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtaacctca 100
gcgatctcaa cgaataggat cttgtgtttg ccgctattcc agttggtgct 150
ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggtat atctggatcc tcctgctgct ggttttggtg 250
 gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300
 gagaccccgga attgattctc acagggcgac catggcagtt tttgctgttg 350
 gagacttgga ctctatttat gggacagaag cagctgtgag tccaactgtt 400
 ggaattcacc ttcaaactca aaccctgac ctatatcctg ttctgctcc 450
 atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500
 caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
 tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
 ggatgttgga aaaaattttg gtcatggaga tgtttaaata gtaaagtagc 700
 aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
 attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
 gtagtttcca tcacatttag gactccactg cagtatacag cacaccattt 850
 tctgctttta actctttcct agcatggggt ccataaaaaat tattataatt 900
 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
 gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100
 tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
 ccaacacggg gagaaaagaa aatttcccct tttacagtaa tgaatgtggc 1200
 ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250
 cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
 gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
 agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
 ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
1				5					10				15	

Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp
 20 25 30
 Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
 35 40 45
 His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu
 50 55 60
 Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
 65 70 75
 Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
 80 85 90
 Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
 95 100 105
 Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
 110 115 120
 Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
 125 130 135
 Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
 140 145

<210> 391
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 391
 cttttcagtg tcacctcagc gatctc 26

<210> 392
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 392
 ccaaaacatg gagcaggaac agg 23

<210> 393
 <211> 47
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

B1
<400> 394
gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50
acccaccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcgggcgga ccbtgacgag aagcccacgg ccagctcagt 200
tctcttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
ctcttcaaaa ctcatctct gggtgactga gttaatagag tggatacaac 300
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtccag aaattgagtt tactgttgct tgtatttgga ctcatgtggg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
gtcaagttac gtgagcaaact actagactta agcaaaagat atgttaaagc 600
tctagcagag gaaaataaga acacagtggg tctcgagaac ggtgcttcta 650
tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700
attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggtgc 800
cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850
ttgaaaatca ccttgtgctg ctccatccac tgtggattat atcctatggc 900
agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950
aagctctaca ctttttcaag gagtatgctg gattcatgga actctaattc 1000
tgtacataaa aatttttaaag ttatttgttt gctttcaggc aagtctgttc 1050
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggg 1100

aagcagatag gtgagttttg tataaatctt ttgtgtttga gatcaagctg 1150
aatgaaaac actgaaaaac atggattcat ttctataaca cttttattta 1200
agtatataac acgttttttg gacaagtga gaagtgttaa tcattctgtc 1250
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tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350
tataatgttg aaaataatgt ttgaaatca tgacccaaag aatgtattga 1400
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acctttatgt gaagaaatta attatatgcc attgccaggt 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5				10					15	

Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
 20 25 30
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
 35 40 45
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
 50 55 60
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
 65 70 75
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
 80 85 90
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
 95 100 105
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
 110 115 120
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
 125 130 135
 Ser Gly Ser Ile Arg
 140

<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 396
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 gggcccagac aaccgcggca tgcttccccg ggtgccaatg cgaggtggag 150
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300
 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
 caccagcatc tcacccactg ctttctcccc ctttcgtac ctggagtcgc 400
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 agctcacccc tgagcgacgt gaaccttagc caacaaccagc tccgggaggt 500
 ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550
 acctctccca caacctcatt caccgcctcg tgccccaccc cacgagggcc 600
 ggcttgctg cgcccacat tcagagcctg aacctggcct ggaaccggct 650

B1

ccatgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700
atgggaaccc tctagctgtc attggtccgg gtgccttcgc ggggctggga 750
ggccttacac acctgtctct ggccagcctg cagaggctcc ctgagctggc 800
gcccagtggc ttccgtgagc taccgggcct gcaggtcctg gacctgtcgg 850
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tgccaggggc ccacatct tgtgacaaat ggtgtggccc agggccacat 1150
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 cccacaggg cagtgaagtc tgtcttcccc cacctgccta gcccatcattc 2550
 tatctaaccg gtccttgatt taataaacac tataaaaggt ttaaaaaaaaa 2600
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 397
 Met Pro Trp Pro Leu Leu Leu Leu Ala Val Ser Gly Ala Gln
 1 5 10 15
 Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr
 20 25 30
 Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
 35 40 45
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
 50 55 60
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
 65 70 75
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
 80 85 90
 Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
 95 100 105
 Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu
 110 115 120
 Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
 125 130 135
 Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
 140 145 150

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser
 155 160 165
 His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly
 170 175 180
 Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg
 185 190 195
 Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu
 200 205 210
 Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe
 215 220 225
 Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln
 230 235 240
 Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly
 245 250 255
 Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala
 260 265 270
 Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp
 275 280 285
 Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
 290 295 300
 His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg
 305 310 315
 Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly
 320 325 330
 Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser
 335 340 345
 Ala Ala Arg Gly Pro Thr Ile Leu
 350

<210> 398
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 398
 ccctgccagc cgagagcttc acc 23

<210> 399
 <211> 23
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga agggtgagct acgttggtt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat tccccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc caciaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga 600

tgctgcctcc tgcgccattt gctaagactc tatctggaca gggatattta 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaattcctt tcttaccatc aagaaggacc tccggtcttc tcatgccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800
 gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850
 gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
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 cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050
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 tatttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200
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 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
 aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
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Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
				20					25				30	
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
				35					40				45	
Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
				50					55				60	
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
				65					70				75	
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
				80					85				90	

Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
 95 100 105
 Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile
 110 115 120
 Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg
 125 130 135
 Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu
 140 145 150
 Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
 155 160 165
 Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe
 170 175 180
 Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser
 185 190 195
 Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu
 200 205 210
 Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys
 215 220 225
 Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln
 230 235 240
 Ala Ala Val Val Lys Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln
 245 250 255
 Trp Met Glu Glu Thr Glu
 260

<210> 403
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 403
 ctccctgtggt ctccagattt caggccta 28

<210> 404
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

B1
<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50
aggcttttgc cgctgacca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactcaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcctat ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tcccctttgg aatcagtc tggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggatgaat gggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggatgaagg attcatgagt ctatataaag 900
gctttttacc atcttggtg agaatagccc cttggtcaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala
 20 25 30
 Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr
 35 40 45
 Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp
 50 55 60
 Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala
 65 70 75
 Leu Gly Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly
 80 85 90
 Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
 95 100 105
 Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser
 110 115 120
 Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met
 125 130 135
 Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
 140 145 150
 Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly
 155 160 165
 Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile
 170 175 180
 Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro
 185 190 195
 Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr
 200 205 210
 Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu
 215 220 225
 Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
 230 235 240
 Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg
 245 250 255
 Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
 260 265 270
 Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
 275 280 285
 Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
 290 295 300
 Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407
<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-31
<223> Synthetic construct.

<400> 407
cgcggatccc gttatcgtct tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<400> 408
gcggaattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
cggacgctg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50
tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100
cagcatttaa tgaaaaatth atgcttaaga agtaaaaatg gcaggcttcc 150
tagataatth tcgttgcca gaatgtgaat gtattgactg gagtgagaga 200
agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300
accatgcctt tcacacatgt ggtgtattht ccacattggc tttcttcatg 350
ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
ctgttttagga agaacagggtg ctcgagtttg gcttttcatt ggtttcatgt 450
tgatgttttg gtcacttatt gcttccatgt ggattcttht tgggtcatat 500
gttaccctaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

380

tgcacttata ttttttagca ctctgatcta caaatttgga agaaccgaag 600
 agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650
 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750
 ttgaaatagt tttatgaaat ttctttattt ttcattgcat agactgttaa 800
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850
 tattcctgag atttagaact tgatctactc cctgagccag ggttacatca 900
 tcttgtcatt ttagaagtaa ccactcttgt ctctctggct gggcacggtg 950
 gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000
 ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
 aggttgacgt gagctgagtt tgcgccactg cactctagcc tgggggagaa 1200
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
 cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
 ttttttggtg aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
 tttatataat gattttttta atgcccaaag gactagtttg aaagcttctt 1450
 ttaaaaagaa ttcctcta atgactttat gtgagaa 1487

<210> 410
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 410
 Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
 1 5 10 15
 Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
 20 25 30
 Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
 35 40 45
 Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
 50 55 60
 Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
 65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
155

<210> 411
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 411
gtttgaggaa gctgggatac 20

<210> 412
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 412
ccaaactcga gcacctgttc 20

<210> 413
<211> 40
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 413
atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414

gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ctttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggccctcatc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtccctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcatgcc cccgaagcca ttttaggggtg gctgtggctc 1000
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
cccggcaggg gctgaggagg aggagcaggg ggtgctgcgt ggaaggtgct 1100
gcaggtcctt gcacgtgtg tcgcgcctct cctcctcgga aacagaaccc 1150
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200
accagctgtc tgtggagaga atgggggtgct ttcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300
tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415

Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
<223> Synthetic construct.

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

B1
<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gtgc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
.gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc 200
ctctctctct gctgtgctta gtctcttagt cctcaaattc ccagtcccct 250
gcaccccttc ctgggacact atgttggttct ccgccctcct gctggagggtg 300
atttggatcc tggctgcaga tgggggtcaa cactggacgt atgaggggccc 350
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtga actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600
cactgggggtc agaaaggatc ccaggggggg tcagaacacc agatcaacag 650
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900
 cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
 gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000
 ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050
 cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100
 tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150
 gtgtaggaat cttggttggc tgtctctgcc ttctcctggc tgtttatattc 1200
 attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250
 cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300
 catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350
 ggggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400
 ccttcccctg gacatctctt agagaggaat ggaccagggc tgtcattcca 1450
 ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500
 gaaatcgctg tgttgttaat gcagaganca aactctgttt agttgcaggg 1550
 gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600
 tttccctaga tatactgcyg gatctctcct taggataaag agttgctggt 1650
 gaagttgtat attttggatc aatatatttg gaaattaaag tttctgactt 1700
 t 1701

<210> 423
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 423
 Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
 1 5 10 15
 Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
 20 25 30
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
 35 40 45
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
 50 55 60
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
 65 70 75
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80 85 90
 Pro Ser Thr Leu Tyr Leu Gly Gly Leu Pro Arg Lys Tyr Val Ala
 95 100 105
 Ala Gln Leu His Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly
 110 115 120
 Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His
 125 130 135
 Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala
 140 145 150
 Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu
 155 160 165
 Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His
 170 175 180
 Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro
 185 190 195
 Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe
 200 205 210
 Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val
 215 220 225
 Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln
 230 235 240
 Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro
 245 250 255
 Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn
 260 265 270
 Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr
 275 280 285
 Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly
 290 295 300
 Cys Leu Cys Leu Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile
 305 310 315
 Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser
 320 325 330
 Ala Gln Ala Thr Thr Glu Ala
 335

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

B1
<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
aattttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgcttt gggactccct cccacaaaac tggctccgga tcaggaaca 200
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaatac 300
 ctgctgcagg aatgacacct ggtaccaga cccaccatt gaccctggga 350
 gggttgaatg tacaacagca actgcacca catgtgttac caattttgt 400
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
 aaatcttcac gagcctcatc atccattcct tgttcccggg aggcacctg 500
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
 agcaggagga gcagggtgaa atcctgccac ccagggaacc ccagcaggcc 600
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatac 700
 agcaaatacga attcagtaag ctgtttcaaa ttttttcaac taagtgcct 750
 cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
 gaaaatatcc ttgaaatttc agaaaatatg ttctatgtag agaataccaa 900
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
 tatgtgcctt ggatgatatg catattaaaa catatttgga aaactggaaa 1000
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429
 <211> 209
 <212> PRT
 <213> Homo sapiens

<400> 429
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg
 1 5 10 15
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
 20 25 30
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
 35 40 45
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
 50 55 60
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
 65 70 75

Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn
 80 85 90
 Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr
 95 100 105
 Gln Leu Gly Ala Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro
 110 115 120
 Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly
 125 130 135
 Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp
 140 145 150
 Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln
 155 160 165
 Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp
 170 175 180
 Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His
 185 190 195
 Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln
 200 205

<210> 430
 <211> 1257
 <212> DNA
 <213> Homo Sapien

<400> 430
 ggagagagggc gcgcgggtga aaggcgcatg gatgcagcct gcggcggcct 50
 cggagcgcg cgagaccaga cgctgaccac gttcctctcc tcggtctcct 100
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35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210

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